

SEQUENCE LISTING

<110> ASAHI KASEI KOGYO KABUSHIKI KAISHA

<120> Novel Gene

<130> X12-1408

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<170> PatentIn Ver. 2.0

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35 40 45

Ala Gly Pro Pro Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln
50 55 60

Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly
65 70 75 80

Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly
85 90 95

Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr
100 105 110

Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro
115 120 125

Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser
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Phe Thr Asn Ser Ala Gly Pro Pro Pro Gly Phe Lys Ser Glu Phe

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Thr Gly Pro Gln Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser

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Ala Phe Thr Gly Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp
80 85 90

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Thr Gly Leu Gly Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn
95 100 105

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Arg Ala Ala Thr Pro Phe Ser Asp Ser Trp Tyr Pro Ser Tyr Pro
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Pro Ser Tyr Pro Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly
125 130 135 140

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Gly Ser Gly Ser Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg
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Thr Ala Ser Gly Tyr Gly Gly Thr Arg Arg Arg
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cctgttaaca attggaaaaa gggatattc aaaagttcgg tggtgtatg tccagtgtag 834

cgttttgtat tctattattt gagggctaaaa gttgatgtgt gacaaaatac ttatgtgttg 894

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<213> Homo sapiens

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35 40 45

Tyr Asp Arg Tyr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu
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Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val
65 70 75 80

Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu
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Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val
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Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly
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Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln
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Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp
145 150 155 160

Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu
165 170 175

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Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro
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Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His
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Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr
245 250 255

Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Ile
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Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp
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Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn
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Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys

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Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp
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cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac tat 261
Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr
35 40 45

gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa 309
Asp Arg Tyr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys
50 55 60 65

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Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile
70 75 80

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Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys
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Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser
100 105 110

tgt gaa ggc tat gag tcc tct gaa gac cag tat gta cta aga ggt tct 501
Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser
115 120 125

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Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gin Lys
 130 135 140 145

ctg aag gag tct gga aag cag cac ggc ttt gcc tct ttc tat gat tat 597
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tat tat aag tgg tcc tcg gcg gat tcc tgt aac atg agt gga ttg att 645
 Tyr Tyr Lys Trip Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile
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 Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe
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 Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro
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cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggc cat ggt 837
 Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly
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gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat gaa 885
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aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta 933
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Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser

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315

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Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Thr Arg

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Arg Arg

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Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val
35 40 45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
50 55 60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
65 70 75 80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
85 90 95

Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe
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cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcacct 180

aaaacattta ttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236

Met Ala Gly Ala

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att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att
Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile
Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile 20

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ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct 332
ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct
Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala
Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala 30 35

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cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat
Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp
Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp 40 45 50

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gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc

Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro
55 60 65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476
Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu
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Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Ser

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Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val
35 40 45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
50 55 60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
65 70 75 80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
85 90 95

Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe
100 105 110

Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu
115 120 125

Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala
130 135 140

Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu

145 150 155 160
Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr

165 170 175
Tyr Glu Cys Asp Val Leu Pro Tyr Ala Gln His Leu His His Tyr Gly

180 185 190
Val Val Leu Glu Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser

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Gly Lys Ser His Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr

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cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcacct 180

aaaacattta ttcaaggag aaaagaaaaa ggggggcgc aaaa atg gct ggg gca 236
Met Ala Gly Ala

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att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284
Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile
5 10 15 20

ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttt att gct 332
Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala
25 30 35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat 380
Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp
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gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc 428
Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro
55 60 65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476
Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu
70 75 80

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Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His
85 90 95 100

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Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu
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Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val
120 125 130

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Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp
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Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe
150 155 160

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aca tct ccc aag act cca gag cat gag ggc cgt tac tat gaa tgt gat
Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp
165 170 175 180

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Val Leu Pro Tyr Ala Gln His Leu His His Tyr Gly Val Val Leu Glu
185 190 195

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Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr Pro Ser Gly Met
215 220 225

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Val Phe His Arg Val

230

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<210> 9

<211> 198

<212> PRT

<213> Homo sapiens

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Ala Ala Lys Asn Phe Glu Asp Val Arg Cys Lys Cys Ile Cys Pro Pro
35 40 45

Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn Ile Ser Gln Lys
50 55 60

Asp Cys Asp Cys Leu His Val Val Glu Pro Met Pro Val Arg Gly Pro
65 70 75 80

Asp Val Glu Ala Tyr Cys Leu Arg Cys Glu Cys Lys Tyr Glu Glu Arg
85 90 95

Ser Ser Val Thr Ile Lys Val Thr Ile Ile Tyr Leu Ser Ile Leu

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105

110

Gly Leu Leu Leu Leu Tyr Met Val Tyr Leu Thr Leu Val Glu Pro Ile

115

120

125

Leu Lys Arg Arg Leu Phe Gly His Ala Gln Leu Ile Gln Ser Asp Asp

130

135

140

Asp Ile Gly Asp His Gln Pro Phe Ala Asn Ala His Asp Val Leu Ala

145

150

155

160

Arg Ser Arg Ser Arg Ala Asn Val Leu Asn Lys Val Glu Tyr Ala Gln

165

170

175

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180

185

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Arg His Val Val Leu Ser

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<213> Homo sapiens

<220>

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Met Ala Thr Leu Trp Gly Gly Leu Leu

1 5

cggttggcc tcc ttg ctc agc ctg tcg tgc ctg gcg ctt tcc gtg ctg 160
Arg Leu Gly Ser Leu Leu Ser Leu Ser Cys Leu Ala Leu Ser Val Leu
10 15 20 25ctg ctg gcg cag ctg tca gac gcc gcc aag aat ttc gag gat gtc aga 208
Leu Leu Ala Gln Leu Ser Asp Ala Ala Lys Asn Phe Glu Asp Val Arg
30 35 40tgt aaa tgt atc tgc cct ccc tat aaa gaa aat tct ggg cat att tat 256
Cys Lys Cys Ile Cys Pro Pro Tyr Lys Glu Asn Ser Gly His Ile Tyr
45 50 55aat aag aac ata tct cag aaa gat tgt gat tgc ctt cat gtt gtg gag 304
Asn Lys Asn Ile Ser Gln Lys Asp Cys Asp Cys Leu His Val Val Glu
60 65 70ccc atg cct gtg cgg ggg cct gat gta gaa gca tac tgt cta cgc tgt 352
Pro Met Pro Val Arg Gly Pro Asp Val Glu Ala Tyr Cys Leu Arg Cys
75 80 85

gaa tgc aaa tat gaa gaa agc tct gtc aca atc aag gtt acc att 400

Glu Cys Lys Tyr Glu Glu Arg Ser Ser Val Thr Ile Lys Val Thr Ile
 90 95 100 105

ata att tat ctc tcc att ttg ggc ctt cta ctt ctg tac atg gta tat 448
 Ile Ile Tyr Leu Ser Ile Leu Gly Leu Leu Leu Tyr Met Val Tyr
 110 115 120

ctt act ctg gtt gag ccc ata ctg aag agg cgc ctc ttt gga cat gca 496
 Leu Thr Leu Val Glu Pro Ile Leu Lys Arg Arg Leu Phe Gly His Ala
 125 130 135

cag ttg ata cag agt gat gat att ggg gat cac cag cct ttt gca 544
 Gln Leu Ile Gln Ser Asp Asp Asp Ile Gly Asp His Gln Pro Phe Ala
 140 145 150

aat gca cac gat gtg cta gcc cgc tcc cgc agt cga gcc aac gtg ctg 592
 Asn Ala His Asp Val Leu Ala Arg Ser Arg Ala Asn Val Leu
 155 160 165

aac aag gta gaa tat gca cag cag cgc tgg aag ctt caa gtc caa gag 640
 Asn Lys Val Glu Tyr Ala Gln Gln Arg Trp Lys Leu Gln Val Gln Glu
 170 175 180 185

cag cga aag tct gtc ttt gac cgg cat gtt gtc ctc agc taattggaa 689
 Gln Arg Lys Ser Val Phe Asp Arg His Val Val Leu Ser
 190 195

ttaattcaa ggtgactaga aagaaacagg cagacaactg gaaagaactg actgggttt 749

gctgggttc atttaatac ctgttgatt tcaccaactg ttgttggaaatccaaaact 809

ggaagcaaaa acttgcttga ttttttttc ttgttaacgt aataatagag acattttaa 869

aagcacacag ctcaaagtca gccaataagt ctttccat ttgtgacttt tactaataaa 929

aataaatctg cctgtaaatt atcttgaagt cctttacctg gaacaaggcac tcttttttc 989

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1498

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<211> 221

<212> PRT

<213> Homo sapiens

<400> 11

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20 25 30

Gln Ala Ala Gly Asp Ala Pro Pro Pro Tyr Ser Ser Ile Ser Ala Glu
35 40 45

Ser Ala Ala Tyr Phe Asp Tyr Lys Asp Glu Ser Gly Phe Pro Lys Pro
50 55 60

Pro Ser Tyr Asn Val Ala Thr Thr Leu Pro Ser Tyr Asp Glu Ala Glu
65 70 75 80

Arg Thr Lys Ala Glu Ala Thr Ile Pro Leu Val Pro Gly Arg Asp Glu
85 90 95

Asp Phe Val Gly Arg Asp Asp Phe Asp Asp Ala Asp Gln Leu Arg Ile
100 105 110

Gly Asn Asp Gly Ile Phe Met Leu Thr Phe Phe Met Ala Phe Leu Phe
115 120 125

Asn Trp Ile Gly Phe Phe Leu Ser Phe Cys Leu Thr Thr Ser Ala Ala

130

135

140

Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu Ile Lys Trp

145 150

155

160

Ile Leu Ile Val Arg Phe Ser Thr Tyr Phe Pro Gly Tyr Phe Asp Gly

165

170

175

Gln Tyr Trp Leu Trp Trp Val Phe Leu Val Leu Gly Phe Leu Leu Phe

180

185

190

Leu Arg Gly Phe Ile Asn Tyr Ala Lys Val Arg Lys Met Pro Glu Thr

195

200

205

Phe Ser Asn Leu Pro Arg Thr Arg Val Leu Phe Ile Tyr

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215

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gctcgctctg cttccctgtc gccggctgcttgc cc atg gcttgc tttgc gcttgc 173
Met Ala Leu Ala Leu Ala Ala

1 5

ctg gcg gcg gtc gag ccg gcc tgc ggc agc cgg tac cag cag ttg cag 221
 Leu Ala Ala Val Glu Pro Ala Cys Gly Ser Arg Tyr Gln Gln Leu Gln
 20

10

15

20

aat gaa gaa gag tct gga gaa cct gaa cag gct gca ggt gat gct cct 269
Asn Glu Glu Glu Ser Gly Glu Pro Glu Gln Ala Ala Gly Asp Ala Pro

25

30

35

cca cct tac agc agc att tct gca gag agc gca gca tat ttt gac tac 317
 Pro Pro Tyr Ser Ser Ile Ser Ala Glu Ser Ala Ala Tyr Phe Asp Tyr
 52 55

40

45

50

aag gat gag tct ggg ttt cca aag ccc cca tct tac aat gta gct aca 365
 Lys Asp Glu Ser Gly Phe Pro Lys Pro Pro Ser Tyr Asn Val Ala Thr
 70

60

65

70

aca ctg ccc agt tat gat gaa gcg gag agg acc aag gct gaa gct act 413
 Thr Leu Pro Ser Tyr Asp Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr

75

80

85

atc cct ttg gtt cct ggg aga gat gag gat ttt gtg ggt cggt gat gat 461
Ile Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp

90 95 100
ttt gat gat gct gac cag ctg agg ata gga aat gat ggg att ttc atg 509
Phe Asp Asp Ala Asp Gln Leu Arg Ile Gly Asn Asp Gly Ile Phe Met
105 110 115

tta act ttt ttc atg gca ttc ctc ttt aac tgg att ggg ttt ttc ctg 557
Leu Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu
120 125 130 135

tct ttt tgc ctg acc act tca gct gca gga agg tat ggg gcc att tca 605
Ser Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser
140 145 150

gga ttt ggt ctc tct cta att aaa tgg atc ctg att gtc agg ttt tcc 653
Gly Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser
155 160 165

acc tat ttc cct gga tat ttt gat ggt cag tac tgg ctc tgg tgg gtg 701
Thr Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val
170 175 180

ttc ctt gtt tta ggc ttt ctc ctg ttt ctc aga gga ttt atc aat tat 749
Phe Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr
185 190 195

gca aaa gtt cggt aag atg cca gaa act ttc tca aat ctc ccc agg acc 797
Ala Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr
200 205 210 215

aga gtt ctc ttt att tat taaagatgtt ttctggcaaa ggccattcctg 845

Arg Val Leu Phe Ile Tyr

220

catttatgaa ttctctctca agaagcaaga gaacacctgc aggaagtgaa tcaagatgca 905

gaacacagag gaataatcac ctgcattaaa aaaataaaagt actgttgaaa agatcatttc 965

tctctatgg ttccttaggtg taaaattttt atagttaatg cagaattctg taatcattga 1025

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gccttatata ttgtttgtag tcattttaa tagcatgagc catgtccctg tagtcgttag 1145

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gatatgtata atgctggcca ttttaaagggttttctcaa aagttaact ttgttatgaa 1265

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actaggatac aaatgaagct taattactaa aatgttaattc ttgacactct ttctataatt 1565

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agaaaaccagt gggttataat gtagaatgtat gtgccttctg cccaaatgggt aattcatctt 1805

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<211> 242

<212> PRT

<213> Homo sapiens

<400> 13

Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn
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Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser
20 25 30

Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu
35 40 45

Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val
50 55 60

Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro
65 70 75 80

Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu
85 90 95

Lys Ala Lys Ala Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln
100 105 110

Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala
115 120 125

Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe
130 135 140

Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile
145 150 155 160

Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu
165 170 175

Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr
180 185 190

Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu
195 200 205

Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg
210 215 220

Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe
225 230 235 240

Leu Leu

<210> 14

<211> 2324

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (13)..(738)

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1 5 10

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Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro

15 20 25

cct act tca aac cca gca ccg cag att gtg cag gct gcg tct tca gca 147
Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala

30 35 40 45

cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act 195
Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr
50 55 60

gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat 243
Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr
65 70 75

ccc gtg cca cct ccc tat agc gtt acc tct ctt cct aca tac gat 291
Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp
80 85 90

gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gaa 339
Glu Ala Glu Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Glu
95 100 105

aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc 387
Thr Ser Gln Arg Ile Gln Glu Glu Cys Pro Pro Arg Asp Asp Phe
110 115 120 125

agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg 435
Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu
130 135 140

gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc 483
Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser
145 150 155

ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga 531
Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly
160 165 170

ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat 579
Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp
175 180 185

tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt 627
Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe
190 195 200 205

ctt gta ctt ggc ctg ctc ctt itc ttc aga gga ttt gtt aat tat cta 675
Leu Val Leu Gly Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu
210 215 220

aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg 723
Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg
225 230 235

tat ttc ttc tta ttg tagagactgc atcaacccga cattcccttc ttataccaaat 778
Tyr Phe Phe Leu Leu
240

gtgaaatttc cagatcatct gtaaacctac aactttaata gaagactact aataacagaa 838

gacaatttag tgaagaaaag acggagttc gaaattgaat ggcagggtgg ttttgctta 898

caagccattt ctgttccattc tttaagtatc tatatttcat ttgtttgca catatgtata 958

tgtgccatt taagatattt gcatatactt gatagaaacc ataaagtgtt agcagtttt 1018

tccagtcaca ttggtaat cagtgttg tataattgaa agagttgagt ggataaacag 1078

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cacacacata tatataattt gaaacgtgag tgttaagat agaatttgtt ttaggacaaa 1498

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acatatccctg aactgagata tgcaaaaatac tcattttcaa gttatggaaa tgggtttgtg 1918

gcatatagga ctgtggggtc tgggtgtt gtagggacta ttataactgg 1978

aatttaattt acattcataa actactatac ttcccatctt gcaaatcatt ttatgcicca 2038

tctgttttc ctttcggta tatcttttgtt ttgaatacc aacatttaaa atgatggat 2098

tttatctttt aaacttaaaa attatataa acagctataa ggacctata aaattgattt 2158

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<211> 242

<212> PRT

<213> Homo sapiens

<400> 15

Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn

1

5

10

15

Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser

20

25

30

Asn Pro Ala Pro Gln Ile Val Gin Ala Val Ser Ser Ala Pro Ala Leu

35

40

45

Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val

50

55

60

Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro

65

70

75

80

Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu

85

90

95

Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln

100

105

110

Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala

115

120

125

Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe

130

135

140

Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile

145

150

155

160

Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu

165

170

175

Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr
180 185 190

Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu
195 200 205

Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg
210 215 220

Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe
225 230 235 240

Leu Leu

<210> 16

<211> 2324

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (13)..(738)

<400> 16

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Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro
15 20 25

cct act tca aac cca gca ccg cag att gtg cag gct gtg tct tca gca 147
Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala
30 35 40 45

cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act 195
Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr
50 55 60

gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat 243
Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr
65 70 75

ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat 291
Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp
80 85 90

gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gaa 339
Glu Ala Glu Lys Ala Ala Ala Ala Met Ala Ala Ala Ala Glu
95 100 105

aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc 387
Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe
110 115 120 125

agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg 435
Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu
130 135 140

gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc 483
Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser
145 150 155

ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga 531
Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly
160 165 170

ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat 579
Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp
175 180 185

tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt 627
Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe
190 195 200 205

ctt gta ctt ggc ctg ctc ctt ttc aga gga ttt gtt aat tat cta 675
Leu Val Leu Gly Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu
210 215 220

aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg 723
Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg
225 230 235

tat ttc ttc tta ttg tagagactgc atcaacccga cattcccttc ttataccaat 778

Tyr Phe Phe Leu Leu

240

gtgaaatttc cagatcatct gtaaacctac aacttataa gaagactact aataacagaa 838

gacaaatitag tgaagaaaag acggagttc gaaattgaat ggcagggtgg ttttgctta 898

caagccattt ctgttcattc ttaagtatac tatatttcat ttgtttgca catatgcata 958

tgtgccatt taagatattt gcataatactt gatagaaacc ataaagttgt agcagttaaag 1018

tccagtcaca tttggtaat cagtgttga tataattgaa agagttgagt ggataaacag 1078

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actaatttta aattaagtga actaaatata tatgtgtata tgtatacaca tatatacaca 1438

cacacacata tatataattta gaaacgtgag tggtaaagat agaatttgtt ttaggacaaa 1498

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aagagatctt gcaggaagag attgtattag atattatatt tatttcattt aagataattt 1678

tcaaagttaa tttcttaat aagataattc tcatttgtt ttgtctttt aaaggccaaat 1738

aaaatatctt tcagtatcat tgtaataatt ttttagagtt taatttgtaa agcttagcaa 1798

ataaaatctt gtactatgaa tagcttcgg ctttagact ttaggattaa ctgtaaaaaa 1858

acatatcctg aactgagata tgcaaaatac tcatttcaa gtatggaaa tgtgtttgtg 1918

gcatatagga ctgtggggtc tgtgtgtgt gtgagagtgt gtgcacta ttataacigg 1978

aatttaattt acattcataa actactatac ttcccatctt gcaaatcatt ttatgtctca 2038

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tttatctttt aaacttaaaa attatataat acagctatac ggacctataa aaattgattt 2158

cttatttattt attagacatt actactaaaa ggtacatcta actattcagg gacattttc 2218

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2324

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<211> 336

<212> PRT

<213> Homo sapiens

<400> 17

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Asn Ala Glu Val Ser Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu
35 40 45

Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Arg Gly Pro
50 55 60

Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly
65 70 75 80

Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp
85 90 95

His His Gln Pro Gly Thr Gly Arg Tyr Gin Val Leu Leu Asn Glu Glu
100 105 110

Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro
115 120 125

Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr

130

135

140

Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr

145

150

155

160

Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro

165

170

175

Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala

180

185

190

Lys Ala Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Cln Arg Ile

195

200

205

Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln

210

215

220

Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala

225

230

235

240

Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn

245

250

255

Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu

260

265

270

Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr

275

280

285

Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu
290 295 300

Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met
305 310 315 320

Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu
325 330 335

<210> 18

<211> 2636

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<220>

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<222> (53)..(1060)

<400> 18

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Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn
5 10 15

agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg 154
agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg

Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala
20 25 30

gag gtc tcg gcg gcc gct gcg gga aca gga agt gaa gag ctt ccg 202
Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro
35 40 45 50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg 250
Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Arg Gly Pro Ala Ala
55 60 65

acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac 298
Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp
70 75 80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac 346
Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His
85 90 95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac 394
Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn
100 105 110

tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg 442
Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro
115 120 125 130

cag att gtg cag gct gtg tct tca gca cca gca ctt gaa act gac tct 490
Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser

135

140

145

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Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser
150 155 160

gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc 586
Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser
165 170 175

gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct 634
Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala
180 185 190

gct gca atg gca gct gca gca gaa aca tct caa aga att cag gag 682
Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu
195 200 205 210

gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga 730
Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg
215 220 225

gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att 778
Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile
230 235 240

ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata 826
Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile
245 250 255

gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa 874
Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys
260 265 270

tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat 922
Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn
275 280 285 290

gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt 970
Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu
295 300 305

ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa 1018
Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu
310 315 320

agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg 1060
Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu
325 330 335

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gtaaaacctac aactttaata gaagactact aataacagaa gacaaatttag tgaagaaaag 1180

acggagtttc gaaattgaat ggcagggtgg ttttgctta caagccattt ctgttccattc 1240

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cagtgttgta tataattgaa agagttgagt ggataaacag tcttcagct tgtaaatgcc 1420

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actaaatata tatgtgtata tgtatacaca tatatataca cacacacata tatatatattt 1780

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accaaatgtc ctttataaga aaaataaatt ttgttttaag ggacatacca gttttaggaa 1900

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actactaaaa ggtacatcta actattcagg gacatttttc catttccaaa aaataaaatt 2560

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2636

acagttttgt ttigct

<210> 19

<211> 336

<212> PRT

<213> Homo sapiens

<400> 19

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Leu Asn Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr

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30

Asn Ala Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu
35 40 45

Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro
50 55 60

Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly
65 70 75 80

Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp
85 90 95

His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu
100 105 110

Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro
115 120 125

Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr
130 135 140

Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr
145 150 155 160

Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro
165 170 175

Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala

180 185 190
Lys Ala Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile
195 200 205
Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln
210 215 220
Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala
225 230 235 240
Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn
245 250 255
Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu
260 265 270
Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr
275 280 285
Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu
290 295 300
Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met
305 310 315 320
Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu
325 330 335

<210> 20

<211> 2636

<212> DNA

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<221> CDS

<222> (53)..(1060)

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Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn

5

10

15

agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg 154
Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala

20

25

30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg 202
Glu Val Ser Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro

35

40

45

50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg 250
Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Arg Gly Pro Ala Ala

55

60

65

acg acg tcg tcg acg ggg gtt gcc gtt gga gct gag cac gga gaa gac 298
Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp

70

75

80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac 346
Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His

85

90

95

cag ccg ggg act ggg cgc tac cag gtt ctt aat gaa gag gat aac 394
Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn
100 105 110

tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg 442
Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro

115

120

125

130

cag att gtt cag gct gct tca gca cca gca ctt gaa act gac tct 490
Gin Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser
135 140 145

tcc cct cca cca tat agt agt att act gtt gaa gta cct aca act tca 538
Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser
150 155 160

gat aca gaa gtt tac ggt gag ttt tat ccc gtt cca cct ccc tat agc 586
Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser
165 170 175

gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct 634
Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala
180 185 190

gct gca atg gca gct gca gca gaa aca tct caa aga att cag gag 682
Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu
195 200 205 210

gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga 730
Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg
215 220 225

gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att 778
Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile
230 235 240

ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata 826
Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile
245 250 255

gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa 874
Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys
260 265 270

tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat 922
Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn
275 280 285 290

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gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt 970
Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu
295 300 305

ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa 1018
Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu
310 315 320

agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg 1060
Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu
325 330 335

tagagactgc atcaacccga cattcccttc ttataccaat gtgaaatttc cagatcatct 1120

gtaaacctac aactttaata gaagactact aataacagaa gacaaatttag tgaagaaaag 1180

acggagtttc gaaattgaat ggcagggtgg ttttgctta caagccattt ctgttcattc 1240

ttaagtatc tatatttcat ttgtttgca catacgata tgtgccatt taagatattt 1300

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cagtgtttga tataatigaa agagttgagt ggataaacag tcttccagct tgtaatgcc 1420

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tgatatttac attattttt aggaaaactc ttcctgtaaa taaccatgca taacttactt 1660

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actaaatata tatgtgtata tgtatacaca tatatacaca cacacacata tatataatttta 1780

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attgtattag atattatatt tatttcattt aagataattt tcaaagttaa tttcttaat 2020

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<210> 21

<211> 76

<212> PRT

<213> Homo sapiens

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Lys Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val
20 25 30

Ser Arg Ile Trp Pro Lys Lys Ala Ile Gin Glu Ser Asn Asp Thr Asn
35 40 45

Lys Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr
50 55 60

Lys Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp
65 70 75

<210> 22

<211> 1085

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (176)..(403)

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cggcctccgc ggtgcctgcc ttgcgtctca gtttggaggatcaagcttg ggaaa atg 178

Met

1

gtg tgc att cct tgt atc gtc att cca gtt ctg ctc tgg atc tac aaa 226
Val Cys Ile Pro Cys Ile Val Ile Pro Val Leu Leu Trp Ile Tyr Lys

5

10

15

aaa ttc ctg gag cca tat ata tac cct ctg gtt tcc ccc ttc gtt agt 274
Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val Ser

20

25

30

cgt ata tgg cct aag aaa gca ata caa gaa tcc aat gat aca aac aaa 322

Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn Lys

35

40

45

ggc aaa gta aac ttt aag ggt gca gac atg aat gga tta cca aca aaa 370
Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr Lys

50

55

60

65

gga cca aca gaa atc tgt gat aaa aag aaa gac taaaagaaatt ttccctaaagg 423
Gly Pro Thr Glu Ile Cys Asp Lys Lys Asp

70

75

accccatcat taaaaaatg gacctgataa tatgaagcat ctcccttgta attgtctcg 483

accttttat ctgagaccgg aattcaggat aggagtctag atatcacct gatactaattc 543

aggaaatata tgatatccgt attaaaaatg tagtttagtta tatttaatga ctcatttc 603

aagtccctt ttctttaatg tagcttcattt gctgtttgaa taatatgatt 663

aaatagaagg ttgtgccag tagacattat gttactaaat cagcacttta aaatcttgg 723

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gatagggaaa aggggaaac ttcgttggaaa aatgaaacat ctgttacatt aatgtctaat 1023

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1085

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<211> 84

<212> PRT

<213> Homo sapiens

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20 25 30

Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile
35 40 45

Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr Trp
50 55 60

Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His Ser
65 70 75 80

Leu Ser Gly Leu

<210> 24

<211> 1593

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (65)..(316)

<400> 24

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Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile

1

5

10

15

ctg ccg gaa att cag aag cca gag agg aag att cag ttt aag gag aaa 157
Leu Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys

20

25

30

gtg ctg tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag 205
Val Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln

35

40

45

att ccc ctg ttt ggg atc atg tct tca gat tca gct gac cct ttc tat 253
Ile Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr

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50

55

60

tgg atg aga gtg att cta gcc tct aac aga ggc aca ttg atg gag cac 301
Trp Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His

65

70

75

tct ctc tct ggc ctt tagggagtcc cctcttagga cagggactgc ccagcagcaa 356
Ser Leu Ser Gly Leu

80

gggcagcaga gtgggtgct aagatcctga ggagctcgag gttcgagct ggcttttagac 416

attgggtggga ccaaggatgt ttgcaggat gcccgtatcc taagaagggg gcctgggggt 476

gcgtgcagcc tgtcggggag accccactct gtgcacctat tggctttctt agctgactct 536

tctcggtggg cttagagtct gcctgtttctt gtagctccg tggtagtcc acttgggtca 596

ttagctctgc caagctgagc ctggccaagc tagtgacaca gacccttgca gtgtatgtccg 656

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caccttctgg gctgaagatc acccagctgt gttcagaatt ttcttactgt gcttaggact 836

gcacgcaagt gagcagacac caccgacttc ctttctgcgt caccagtgtc gtcaagcagag 896

agaggacagc acaggctcaa ggttggtagt gaagtcagg tggggctgtgg 956

tggtggtgat cagttgc tcc agt gttt gaa ataagaagac tcatgtttat gtctggaata 1016

agttctgttt gtgc tgacag gtgaccc tgc tggc a cttgct agccaggaaa cagagt gacc 1076

aagggacaag aagggactt g ctaa agcc a cccagcaact cagcagcaga accaagatgg 1136

gccccaggct cctccatatg gcccccaggct taccacccta tcacacgtgg ccttgc ttag 1196

acccagtcct gaggcagggaa gaggctctt g agacc t gatg ccctcctacc cacatggttc 1256

tcccactgcc ctgtctgctc tgctgctaca gagggcagg gcctccccca gcccacgctt 1316

aggaatgctt ggcctctggc aggca ggccag cttgctt gacccaa gctgg tggc agggggctgg 1376

aaggcaccag gcctcaggag gagccccata gtcccgctg cagcctgtaa ccatcggtg 1436

ggccctgcaa gcccacact c acgccc t gttt gatggt cacgg tgggt ggtt gggggc 1496

tgacccca g tccagg gga ctgtcactgt ggacgcca a atggcataac t gataagg 1556

tgaataagt g acaataaag ccagttttt acaagg t 1593

<210> 25

<211> 179

<212> PRT

<213> Homo sapiens

<400> 25

Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu
1 5 10 15

Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val
20 25 30

Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile
35 40 45

Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Val His Ala
50 55 60

Val Val Tyr Ile Val Phe Met Leu Gly Ser Cys Ala Phe Phe Ser Lys
65 70 75 80

Thr Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln
85 90 95

Leu Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met
100 105 110

Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Phe Gly Gly
115 120 125

Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile
130 135 140

Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr

145 150 155 160
Phe Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala

165 170 175

Leu Leu Phe

<210> 26

<211> 1820

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (114)..(650)

<400> 26

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acgcggagca gagctgagct gaagcgggac ccggagcccg agcagccgcc gcc atg 116
Met

1

gca atc aaa ttt ctg gaa gtc atc aag ccc ttc tgt gtc atc ctg ccg 164
Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu Pro

5 10 15

gaa att cag aag cca gag agg aag att cag ttt aag gag aaa gtg ctg 212
Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val Leu
20 25 30

tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag att ccc 260
Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile Pro
35 40 45

ctg ttt ggg atc atg tct tca gat tca gct gac ccg gtc cat gca gtt 308
Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Val His Ala Val
50 55 60 65

gta tac ata gtg ttc atg ctg ggc tcc tgt gca ttc ttc tcc aaa acg 356
Val Tyr Ile Val Phe Met Leu Gly Ser Cys Ala Phe Phe Ser Lys Thr
70 75 80

tgg att gag gtc tca ggt tcc tct gcc aaa gat gtt gca aag cag ctg 404
Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln Leu
85 90 95

aag gag cag cag atg gtg atg aga ggc cac cga gag acc tcc atg gtc 452
Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met Val
100 105 110

cat gaa ctc aac cgg tac atc ccc aca gcc gcg gcc ttt ggt ggg ctg 500
His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Phe Gly Gly Leu
115 120 125

tgc atc ggg gcc ctc tcg gtc ctg gct gac ttc cta ggc gcc att ggg 548

Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile Gly
130 135 140 145.

tct gga acc ggg atc ctg ctc gca gtc aca atc atc tac cag tac ttt 596
Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr Phe
150 155 160

gag atc ttc gtt aag gag caa agc gag gtt ggc agc atg ggg gcc ctg 644
Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala Leu
165 170 175

ctc ttc tgagcccgta tcccgacag gttgaggaag ctgtccaga agccgcctcg 700
Leu Phe

aaggagact ctcatcatgg cgccgtgtgc tgccatata gactttaa taatgtttt 760

gaatttcgta ttcttcatt ccactgtgta aagtctaga cattttccaa tttaaaattt 820

tgcttttat cctggcactg gcaaaaagaa ctgtgaaagt gaatttatic agccgactgc 880

cagagaagtg ggaatggat aggatgtcc ccaagtgtcc atgtaacttt tgtttaacc 940

tttgcacatt ctcaatgttg tatgcggctg cagccgtctc acctgtttcc ccacaagg 1000

aatttctcac tctgggttggaa agcacaaaca ctgaaatgtc tacgtttcat tttggcagta 1060

gggtgtgaag ctgggagcag atcatgtatt tcccgagac atgggacatt gctggcatgt 1120

ctccatcaca atcaggcgtg ggaatatctg gcttaggact gtttctct aagacaccat 1180

tgtttccct tatttaaaa gtgattttt taaggacaga acttcttcca aaagagaggg 1240

atggcttcc cagaagacac tctggagacc ttgcgtggcag tgctagccag gaaacagagt 1300

gaccaaggga caagaaggga ctgcctaaa gccacccagc aactcagcag cagaacccaag 1360

atgggccccca ggctcctcca tatggcccag ggcttaccac cctatcacac gtggccttgt 1420

ctagaccagg tcctgagcag gggagagggct ttgagacct gatgccctcc tacccacatg 1480

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gctggccct gcaaggccca cactcacgccc ctgtgggtga tggcacggg gggtggtgg 1720

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aaggtaata agtacaaat aaagccagtt tttacaagg 1820

<210> 27

<211> 279

<212> PRT

<213> Homo sapiens

<400> 27

Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp
1 5 10 15

Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr
20 25 30

Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg
35 40 45

Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val
50 55 60

Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe
65 70 75 80

Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val
85 90 95

Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp
100 105 110

Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe
115 120 125

Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His
130 135 140

His Ser Val Leu Pro Trp Ser Trp Trp Gly Val Lys Ile Ala Pro

145 150 155 160
Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val

165 170 175
Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln

180 185 190
Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln

195 200 205
Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser
210 215 220

225 230 235 240
Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly

245 250 255
Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr

260 265 270
Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly

Ile Ala Lys Val Lys Ala Asn

275

<210> 28

<211> 1472

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119).. (955)

<400> 28

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tgctccctcc gagcgctccg ccgttgcggc cctggccct acggagtccct tagccagg 118

atg gag gct gtt gtg aac ttg tac caa gag gtg atg aag cac gca gat 166
Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp

1 5 10 15

ccc cgg atc cag ggc tac cct ctg atg ggg tcc ccc ttg cta atg acc 214

Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr

20 25 30

tcc att ctc ctg acc tac gtg tac ttc gtt ctc tca ctt ggg cct cgc 262

Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg

35 40 45

atc atg gct aat cgg aag ccc ttc cag ctc cgt ggc ttc atg att gtc 310

Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val

50 55 60

tac aac ttc tca ctg gtg gca ctc tcc tac att gtc tat gag ttc 358

tat aac ttc tca ctg gtg gca ctc tcc tac att gtc tat gag ttc

Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe
65 70 75 80

ctg atg tcg ggc tgg ctg agc acc tat acc tgg cgc tgt gac cct gtg 406
Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val
85 90 95

gac tat tcc aac agc cct gag gca ctt agg atg gtt cgg gtg gcc tgg 454
Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp
100 105 110

ctc ttc ctc ttc tcc aag ttc att gag ctg atg gac aca gtg atc ttt 502
Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe
115 120 125

att ctc cga aag aaa gac ggg cag gtg acc ttc cta cat gtc ttc cat 550
Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His
130 135 140

cac tct gtg ctt ccc tgg agc tgg tgg ggg gta aag att gcc ccg 598
His Ser Val Leu Pro Trp Ser Trp Trp Gly Val Lys Ile Ala Pro
145 150 155 160

gga gga atg ggc tct ttc cat gcc atg ata aac tct tcc gtg cat gtc 646
Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val
165 170 175

ata atg tac ctg tac tac gga tta tct gcc ttt ggc cct gtg gca caa 694
Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln

180 185 190
ccc tac ctt tgg tgg aaa aag cac atg aca gcc att cag ctg atc cag 742
Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln

195 200 205
ttt gtc ctg gtc tca ctg cac atc tcc cag tac tac ttt atg tcc agc 790
Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser

210 215 220
tgt aac tac cag tac cca gtc att att cac ctc atc tgg atg tat ggc 838
Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly
225 230 235 240
acc atc ttc ttc atg ctg ttc aac ttc tgg tat cac tct tat acc 886
Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr

245 250 255
aag ggc aag cgg ctg ccc cgt gca ctt cag caa aat gga gct cca ggt 934
Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly
260 265 270
att gcc aag gtc aag gcc aac tgagaaggcat ggcttagata ggcccccacc 985

Ile Ala Lys Val Lys Ala Asn
275
taagtgcctc aggactgcac cttagggcag tgtccgtcag tgccctctcc acctacacct 1045

gtgaccaagg cttatgtggt caggactgag caggggactg gccctccccct ccccacagct 1105

gctctacagg gaccacggct ttggttccctc acccacttcc cccgggcagc tccagggatg 1165

tggcctcatt gctgtctgcc actccagagc tggggctaa aagggtgtt cagttatttc 1225

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tcctccaccc cacacactga agcagtagct tctggccaa aggtcagggt gggcggggc 1405

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1472

ggaaacc

<210> 29

<211> 137

<212> PRT

<213> Homo sapiens

<400> 29

Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu

1

5

10

15

Ser Val Val Thr Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu

20

25

30

Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Ser

35

40

45

Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro

50

55

60

Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln

65

70

75

80

Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr

85

90

95

Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly

100

105

110

Gly Ala Ala Ala Pro Tyr Pro Ala Ser Gln Pro Pro Tyr Asn Pro Ala

115

120

125

Tyr Met Asp Ala Pro Lys Ala Ala Leu

130

135

<210> 30

<211> 1788

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (145)..(555)

<400> 30

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ggaaattgaa actgagtgcc ccacgatggg aagaggggaa agcccagggg tacaggagggc 120

ctctgggtga aggtagggc taac atg ggg ttc gga gcg acc ttg gcc gtt 171
Met Gly Phe Gly Ala Thr Leu Ala Val

1 5

ggc ctg acc atc ttt gtg ctg tct gtc act atc atc tgc ttc 219
Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys Phe
10 15 20 25acc tgc tcc tgc tgc ctt tac aag acg tgc cgc cga cca cgt ccg 267
Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg Pro
30 35 40gtt gtc acc acc aca tcc acc act gtg gtg cat gcc cct tat cct 315
Val Val Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr Pro
45 50 55cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag ggc 363
Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln Gly
60 65 70tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac cca 411
Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr Pro
75 80 85

atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg gcc 459
Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro Ala
90 95 100 105

tac cac gag acc ctg gct gga gga gca gca gcc gcg ccc tac ccc gcc agc 507
Tyr His Glu Thr Leu Ala Gly Gly Ala Ala Ala Pro Tyr Pro Ala Ser
110 115 120

cag cct cct tac aac ccg gcc tac atg gat gcc ccg aag gcg gcc ctc 555
Gln Pro Pro Tyr Asn Pro Ala Tyr Met Asp Ala Pro Lys Ala Ala Leu
125 130 135

tgagcattcc ctggcctctc tggctgccac ttggttatgt tgttgtgtg cgtgagtggt 615

gtgcaggcgc ggttccttac gccccatgtg tgctgtgtgt gtccaggcac ggttccttac 675

gccccatgtg tgctgtgtgt gtccctgcctg tatatgtggc ttccctctgat gctgacaagg 735

tggggAACAA tccttgccAG agtgggtgg gaccagactt tttttttttc ctcacctgaa 795

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caagttggac ttgtatccctt tggcagatg tccattgtct ccctggagcc ttcatacgct 1155

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tgagtcctg ctccccgaca ccagcctcat ggaatatgc acaactcctg tacccagtc 1575

cacggtgttc tggcagcagg gacacctggg ccaatgggcc atctggacca aaggtgggtt 1635

gtggggccct ggatggcagc tctggccag acatgaatac ctctgtttcc tcctccctct 1695

attactgttt caccagagct gtcttagctc aaatctgttg tgtttctgag tctagggtct 1755

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1788

<210> 31

<211> 118

<212> PRT

<213> Homo sapiens

<400> 31

Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu
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Ser Val Val Thr Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu
20 25 30

Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Ser
35 40 45

Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro
50 55 60

Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln
65 70 75 80

Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr
85 90 95

Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly
100 105 110

Glu Cys Pro Cys Gln Leu

115

<210> 32

<211> 1908

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91).. (444)

<400> 32

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ggaggccctct gggtaaggc agaggcta ac atg ggg ttc gga gcg acc ttg gcc 114
Met Gly Phe Gly Ala Thr Leu Ala

1

5

gtt ggc ctg acc atc ttt gtg ctg tct gtc act atc atc atc tgc 162
Val Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys

10

15

20

ttc acc tgc tcc tgc tgc ctt tac aag acg tgc cgc cga cca cgt 210
Phe Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg

25

30

35

40

ccg gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat 258
Pro Val Val Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr

45

50

55

cct cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag 306
cct cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag

Pro Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln
60 65 70

ggc tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac 354
Gly Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr
75 80 85

cca atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg 402
Pro Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro
90 95 100

gcc tac cac gag acc ctg gct ggt gag tgc ccc tgc caa ctc 444
Ala Tyr His Glu Thr Leu Ala Gly Glu Cys Pro Cys Gln Leu
105 110 115

tagccctgcc cgacttcccc agtctctgcc agcatccctc gggcacccat cccaaactac 504

atcactcaac aggccctctgc ccctttctgc ttgcctgccca ctcacacggc agcccaccat 564

gctcacagcc aaccagggtc ctctctgtt tcaggaggag cagccgcgcc ctaccccgcc 624

agccagccctc ttacaaccc ggcctacatg gatccccga aggccgcctc ctgagcattc 684

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cggttcctta cgccccatgt gtgcgtgtg tgccaggca cggttcctta cgccccatgt 804

gtgctgtgtg tgtcctgct gtatatgtgg cttcctctga tgctgacaag gtggggaca 864

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ccctgggtt gtggagggaa attggctcag agatggacaa cctggcaact gtgagtcct 1644

gcttcccgac accagccctca tggaaatatgc aacaactcct gtaccccaagt ccacgggttt 1704

ctggcagcag ggacacccctgg gcctaattggc catctggacc aaaggtgggg tgtggggccc 1764

tggatggcag ctctggccca gacatgaata cctcggttc ctccctccctc tattactgtt 1824

tcaccagagc tgtcttagct caaatctgtt gtgtttctga gtctagggtc tgtacacttg 1884

tttataataa atgcaatcgt ttgg

1908

<210> 33

<211> 168

<212> PRT

<213> Homo sapiens

<400> 33

Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro Val Gln
1 5 10 15

Pro Pro Gly Asn Pro Val Tyr Pro Gln Thr Leu His Leu Pro Gln Ala
20 25 30

Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr Arg Pro
35 40 45

Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser Ala Ala
50 55 60

Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val Ala Val
65 70 75 80

Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val Gly Pro
85 90 95

Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr Asp Ala
100 105 110

Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro Pro Pro
115 120 125

Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met Gln Gly
130 135 140

Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met Gly Gly
145 150 155 160

Ser Asp Gly Gly Tyr Thr Ile Trip
165

<210> 34

<211> 1897

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70) .. (573)

<400> 34

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gcaaccacc atg aac agc aaa ggt caa tat cca aca cag cca acc tac cct 111
Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro

1

5

10

gtg cag cct cct ggg aat cca gta tac cct cag acc ttg cat ctt cct 159
Val Gln Pro Pro Gly Asn Pro Val Tyr Pro Gln Thr Leu His Leu Pro
15 20 25 30

cag gct cca ccc tat acc gat gct cca cct gcc tac tca gag ctc tat 207
Gln Ala Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr
35 40 45

cgt ccg agc ttt gtg cac cca ggg gct gcc aca gtc ccc acc atg tca 255
Arg Pro Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser
50 55 60

gcc gca ttt cct gga gcc tct ctg tat ctt ccc atg gcc cag tct gtg 303
Ala Ala Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val
65 70 75

gct gtt ggg cct tta ggt tcc aca atc ccc atg gct tat tat cca gtc 351
Ala Val Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val
80 85 90

ggt ccc atc tat cca cct ggc tcc aca gtg ctg gtg gaa gga ggg tat 399
Gly Pro Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr
95 100 105 110

gat gca ggt gcc aga ttt gga gct ggg gct act gct ggc aac att cct 447
Asp Ala Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro
115 120 125

cct cca cct cct gga tgc cct ccc aat gct gct cag ctt gca gtc atg 495
Pro Pro Pro Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met
130 135 140

cag gga gcc aac gtc ctc gta act cag cgg aag ggg aac ttc ttc atg 543
Gln Gly Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met
145 150 155

ggg ggt tca gat ggt ggc tac acc atc tgg tgaggaacca aggccaccc 593
Gly Gly Ser Asp Gly Gly Tyr Thr Ile Trp
160 165

tgtgccggga aagacatcac atacccctcgacttccatc aatgtaaatgg cttagtcat 653

attaacctga agttgcaggta tagacacatgg ttgttggtt gtccttctgg tgcccaaact 713

ttcaggcact ttccaaatgg aataaggaac catgtatgg tagcagtacc tccctaaagc 773

attttgggtt agggaggta tccattcata aaatgtatgg gggtgaagcc gccctaagga 833

ttttccctta atttcctgg agtaataatgg taccataatgg gtctttgtttt ttagtaataa 893

aacatcaaat taggtttggaa gggaaatgg atccctaa gaattaaatgt tgccaaatta 953

01- 3-26; 7:31PM; 平木国际特许事务所

ttctgattgg tccttaatct cccttaagtc tttgatataat attacttggta ataaatggaa 1013

cgcatttagtt gtcigccctt tccttccat cccttgcccc acccateccca tctccaaccc 1073

tagtcttcca tttcctcccg ccagtctcca ttgaatcaat ggtgcaggac agaaagccag 1133

tcagactaat ttcccttcttt cctcgactt ctccccactc gtcatcttt aactagtgtt 1193

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tcgtatctcc tcaggcaaaa gtggagggtg ccttatggc cctccctata ggttgtctt 1313

gcatacacga acctaaccctt aatttgcctt ggtgccagaa aaactgagct atgtttgaac 1373

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ggaggatgca ttcaaaagc ttgattgtg tggtagc taaattaaga ggagtttca 1493

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tgagtcagt gaaatctcat tagggtttaa gaatatttca gggatcctta atgtttgtat 1673

ttttgttttc tgaaattgga ttttattttta ttttatctta taatttcagt tcatctaaat 1733

tgtgtgttct gtacatgtga tggttgactg taccattgac tggtatggaa gtcagcggtt 1793

gtatgtctct ctctacactg tggtgcactt aacctgtgga attttatac taaaaatgta 1853

gaataaaagac tattttgaag atttgaataa agtgatgaag ttgc

1897

<210> 35

<211> 455

<212> PRT

<213> Homo sapiens

<400> 35

Met Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu
1 5 10 15

Phe Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp
20 25 30

Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe
35 40 45

Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly
50 55 60

Val Leu Asn Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys
65 70 75 80

Val Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr
85 90 95

Phe Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe

100 105

110

Ser Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly

115 120 125

Asp Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu

130 135 140

Gln Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu
145 150 155 160Leu Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr
165 170 175Phe Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg
180 185 190Leu Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala
195 200 205Met Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro
210 215 220Ser Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly
225 230 235 240Ser Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu
245 250 255

Leu Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys
260 265 270

Glu Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe
275 280 285

Leu Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala
290 295 300

Thr Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr
305 310 315 320

Arg Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val
325 330 335

Lys Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile
340 345 350

Val Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr
355 360 365

Ala Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala
370 375 380

Gln Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met
385 390 395 400

Ser Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu
405 410 415

Leu Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val
420 425 430

Ser Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala
435 440 445

Pro Glu Lys Gln Met Ala Pro
450 455

<210> 36

<211> 1903

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (116)..(1480)

<400> 36

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tgctgtggcc tcggggatgt ggaatggag gcaggaggct tccttacact tcgcc atg 118
Met

I

agt ttc ctc atc gac tcc agc atc atg att acc tcc cag ata cta ttt 166
Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu Phe

5 10 15
ttt gga ttt ggg tgg ctt ttc atg cgc caa ttg ttt aaa gac tat 214
Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp Tyr
20 25 30

gag ata cgt cag tat gtt gta cag gtg atc ttc tcc gtg acg ttt gca 262
Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe Ala
35 40 45

ttt tct tgc acc atg ttt gag ctc atc atc ttt gaa atc tta gga gta 310
Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly Val
50 55 60 65

ttg aat agc agc tcc cgt tat ttt cac tgg aaa atg aac ctg tgt gta 358
Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys Val
70 75 80

att ctg ctg atc ctg gtt ttc atg gtg cct ttt tac att ggc tat ttt 406
Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr Phe
85 90 95

att gtg agc aat atc cga cta ctg cat aaa caa cga ctg ctt ttt tcc 454
Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Phe Ser
100 105 110

tgt ctc tta tgg ctg acc ttt atg tat ttc ttc tgg aaa cta gga gat 502
Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly Asp
115 120 125

ccc ttt ccc att ctc agc cca aaa cat ggg atc tta tcc ata gaa cag 550
Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu Gln
130 135 140 145

ctc atc agc cgg gtt ggt gtg att gga gtg act ctc atg gct ctt ctt 598
Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu
150 155 160

tct gga ttt ggt gct gtc aac tgc cca tac act tac atg tct tac ttc 646
Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe
165 170 175

ctc agg aat gtg act gac acg gat att cta gcc ctg gaa cgg cga ctg 694
Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu
180 185 190

ctg caa acc atg gat atg atc ata agc aaa aag aaa agg atg gca atg 742
Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala Met
195 200 205

gca cgg aga aca atg ttc cag aag ggg gaa gtg cat aac aaa cca tca 790
Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro Ser
210 215 220 225

ggt ttc tgg gga atg ata aaa agt gtt acc act tca gca tca gga agt 838
Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly Ser
230 235 240

gaa aat ctt act ctt att caa cag gaa gtg gat gct ttg gaa gaa tta 886
Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu Leu
245 250 255

agc agg cag ctt ttt ctg gaa aca gct gat cta tat gct acc aag gag 934
Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys Glu
260 265 270

aga ata gaa tac tcc aaa acc ttc aag ggg aaa tat ttt aat ttt ctt 982
Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe Leu
275 280 285

ggc tac ttt ttc tct att tac tgt gtt tgg aaa att ttc atg gct acc 1030
Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala Thr
290 295 300 305

atc aat att gtt ttt gat cga gtt ggg aaa acg gat cct gtc aca aga 1078
Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr Arg
310 315 320

ggc att gag atc act gtg aat tat ctg gga atc caa ttt gat gtg aag 1126
Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val Lys
325 330 335

ttt tgg tcc caa cac att tcc ttc att ctt gtt gga ata atc atc gtc 1174
Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Val
340 345 350

aca tcc atc aga gga ttg ctg atc act ctt acc aag ttc ttt tat gcc 1222
aca tcc atc aga gga ttg ctg atc act ctt acc aag ttc ttt tat gcc

Thr Ser Ile Arg Gly Leu Leu Thr Leu Thr Lys Phe Phe Tyr Ala

355

360

365

atc tct agc agt aag tcc tcc aat gtc att gtc ctg cta tta gca cag 1270
Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Ala Gln

370

375

380

385

ata atg ggc atg tac ttt gtc tcc tct gtg ctg ctg atc cga atg agt 1318
Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met Ser
390 395 400

atg cct tta gaa tac cgc acc ata atc act gaa gtc ctt gga gaa ctg 1366
Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu Leu
405 410 415

cag ttc aac ttc tat cac cgt tgg ttt gat gtg atc ttc ctg gtc agc 1414
Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser
420 425 430

gct ctc tct agc ata ctc ttc ctc tat ttg gct cac aaa cag gca cca 1462
Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala Pro
435 440 445

gag aag caa atg gca cct tgaacttaag cctactacag actgttagag 1510
Glu Lys Gln Met Ala Pro
450 455

gccagtggtt tcaaaattta gatataagag gggggaaaaa tggaccagg gcctgacatt 1570

ttataaaca acaaaatgct atggtagcat tttcacctt catagcatac tccttcgg 1630

tcaggtgata ctatgaccat gagtagcatc agccagaaca tgagagggag aactaactca 1690

agacaatact cagcagagag catcccgtgt ggatatgagg ctggtgtaga ggccggagagg 1750

agccaagaaa ctaaaggtaaaaatacact ggaactctgg ggcaagacat gtctatggta 1810

gctgagccaa acacgttagga ttcccgaaaaagttcaca tggaaaaggt tatagcctt 1870

ccttgagatt gactcattaa aatcagagac tgt 1903

<210> 37

<211> 322

<212> PRT

<213> Homo sapiens

<400> 37

Met Ser Ser Leu Gly Gly Ser Gln Asp Ala Gly Ser Ser Ser

1

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10

15

Ser Ser Thr Asn Gly Ser Gly Ser Ser Gly Pro Lys Ala

20

25

30

Gly Ala Ala Asp Lys Ser Ala Val Val Ala Ala Ala Pro Ala Ser

35

40

45

Val Ala Asp Asp Thr Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile

50 55 60

Ile Ser Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser
65 70 75 80

His Tyr Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Ser Met
85 90 95

Met Gly Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala
100 105 110

Ser Leu Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp
115 120 125

Lys Ser Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu
130 135 140

Leu Ser Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu
145 150 155 160

Thr Leu Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val
165 170 175

Gln Glu His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp
180 185 190

Met Glu Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe
195 200 205

Pro Tyr Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr
210 215 220

Pro Ala Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu
225 230 235 240

Ala Glu Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly
245 250 255

Lys Lys Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg
260 265 270

Ile Asn Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His
275 280 285

Gln Ile Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Pro Ser
290 295 300

Ala Ala Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp
305 310 315 320

Phe Gln

<210> 38

<211> 1448

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (292).. (1257)

<400> 38

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ccctgccccg cccctccccc tcggcctcgc ggcgacggcg gcgggtggcggtt ctggacgac 120

tcggagagcc gagtgaaagac atttccacctt ggacacctga ccatgtgcctt gcccgtggca 180

gcgaggccca ccaggcatctt ctgttgtggg cagcagggcc aggtcccttgtt ctgtggaccc 240

tcggcagtggc gagggctccc tctgcagtgg ggtctggcc tcggcccccac c atg tgc 297
Met Ser

1

agc ctc ggc ggt ggc tcc cag gat gcc ggc agt agc agc agc agc 345
Ser Leu Gly Gly Ser Gln Asp Ala Gly Ser Ser Ser Ser Ser

5

10

15

acc aat ggc agc ggt ggc agt ggc agc aag gca gga gca 393
Thr Asn Gly Ser Gly Ser Ser Gly Pro Lys Ala Gly Ala

20

25

30

gca gac aag agt gca gtg gtg gct gcc gca cca gcc tca gtg gca 441
Ala Asp Lys Ser Ala Val Val Ala Ala Ala Pro Ala Ser Val Ala

35

40

45

50

gat gac aca cca ccc ccc gag cgt cgg aac aag agc ggt atc atc agt 489
Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile Ile Ser
55 60 65

gag ccc ctc aac aag agc ctg cgc cgc tcc cgc ccg ctc tcc cac tac 537
Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser His Tyr
70 75 80

tct tct ttt ggc agc agt ggt agt ggc ggt ggc agc atg atg ggc 585
Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Ser Met Met Gly
85 90 95

gga gag tct gac aag gcc act gcg gct gca gcc gct gcc tcc ctg 633
Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ser Leu
100 105 110

ttg gcc aat ggg cat gac ctg gcg gcg gcc atg gcg gtg gac aaa agc 681
Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp Lys Ser
115 120 125 130

aac cct acc tca aag cac aaa agt ggt gct gtg gcc agc ctg ctg agc 729
Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu Leu Ser
135 140 145

aag gca gag cgg gcc acg gag ctg gca gcc gag gga cag ctg acg ctg 777
Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu Thr Leu
150 155 160

cag cag ttt gcg cag tcc aca gag atg ctg aag cgc gtg gtg cag gag 825
Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val Gln Glu
165 170 175

cat ctc ccg ctg atg agc gag gcg ggt gct ggc ctg cct gac atg gag 873
His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp Met Glu
180 185 190

gct gtg gca ggt gcc gaa gcc ctc aat ggc cag tcc gac ttc ccc tac 921
Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe Pro Tyr
195 200 205 210

ctg ggc gct ttc ccc atc aac cca ggc ctc ttc att atg acc ccg gca 969
Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr Pro Ala
215 220 225

ggt gtg ttc ctg gcc gag agc gcg ctg cac atg gcg ggc ctg gct gag 1017
Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu Ala Glu
230 235 240

tac ccc atg cag gga gag ctg gcc tct gcc atc agc tcc ggc aag aag 1065
Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly Lys Lys
245 250 255

aag cgg aaa cgc tgc ggc atg tgc gcg ccc tgc cgg cgg cgc atc aac 1113
Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg Ile Asn
260 265 270

tgc gag cag tgc agc agt tgt agg aat cga aag act ggc cat cag att 1161

tgc aaa ttc aga aaa tgt gag gaa ctc aaa aag aag cct tcc gct gct
 Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser Ala Ala
 295 300 305

1257

ctg gag aag gtg atg ctt ccg acg gga gcc gcc ttc cggtgg ttt cag
 Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp Phe Gln
 310 315 320

tgacggccgc ggaacctaaa gctgccctct ccgtgcaatg tcactgctcg tgtggtctcc 1317

agcaaggat tcgggcgaag acaaacggat gcacccgtct ttagaacc aaatattctc 1377

tcacagatt cattcctgtt ttatata tatttttgt tgctgttta acatctccac 1437

gtacctagca t

〈2,10〉 39

〈211〉 313

212 PRT

<213> Homo sapiens

<400> 39

<400> 39 Met Ala Gly Gln Pro Gly His Met Pro His Gly Gly Ser Ser Asn Asn
10 15

1

5

10

15

Leu Cys His Thr Leu Gly Pro Val His Pro Pro Asp Pro Gln Arg His
20 25 30

Pro Asn Thr Leu Ser Phe Arg Cys Ser Leu Ala Asp Phe Gln Ile Glu
35 40 45

Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val Tyr Lys Ala Thr Cys
50 55 60

Leu Leu Asp Arg Lys Thr Val Ala Leu Lys Lys Val Gln Ile Phe Glu
65 70 75 80

Met Met Asp Ala Lys Ala Arg Gln Asp Cys Val Lys Glu Ile Gly Leu
85 90 95

Leu Lys Gln Leu Asn His Pro Asn Ile Ile Lys Tyr Leu Asp Ser Phe
100 105 110

Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu Leu Ala Asp Ala Gly
115 120 125

Asp Leu Ser Gln Met Ile Lys Tyr Phe Lys Lys Gln Lys Arg Leu Ile
130 135 140

Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln Leu Cys Ser Ala Val
145 150 155 160

Glu His Met His Ser Arg Arg Val Met His Arg Asp Ile Lys Pro Ala
165 170 175

Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys Leu Gly Asp Leu Gly
180 185 190

Leu Gly Arg Phe Phe Ser Ser Glu Thr Thr Ala Ala His Ser Leu Val
195 200 205

Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His Glu Asn Gly Tyr
210 215 220

Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu Leu Tyr Glu Met
225 230 235 240

Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met Asn Leu Phe Ser
245 250 255

Leu Cys Gln Lys Ile Glu Gln Cys Asp Tyr Pro Pro Leu Pro Gly Glu
260 265 270

His Tyr Ser Glu Lys Leu Arg Glu Leu Val Ser Met Cys Ile Cys Pro
275 280 285

Asp Pro His Gln Arg Pro Asp Ile Gly Tyr Val His Gln Val Ala Lys
290 295 300

Gln Met His Ile Trp Met Ser Ser Thr
305 310

<210> 40

<211> 1597

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (153)..(1091)

<400> 40

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ctccagccgc ccgcgggcca ggcacccggt cccccagcgg cagccgagcc cgcccgccgc 120

ccgttcgtgc cctcgtgagg ctggcatgca gg atg gca gga cag ccc ggc cac 173
Met Ala Gly Gln Pro Gly His

1 5

atg ccc cat gga ggg agt tcc aac aac ctc tgc cac acc ctg ggg cct 221
Met Pro His Gly Gly Ser Ser Asn Asn Leu Cys His Thr Leu Gly Pro

10 15 20

gtg cat cct cct gac cca cag agg cat ccc aac acg ctg tct ttt cgc 269
Val His Pro Pro Asp Pro Gln Arg His Pro Asn Thr Leu Ser Phe Arg

25 30 35

tgc tgc ctg gcg gac ttc cag atc gaa aag aag ata ggc cga gga cag 317
Cys Ser Leu Ala Asp Phe Gln Ile Glu Lys Lys Ile Gly Arg Gly Gln

40 45 50 55

ttc agc gag gtg tac aag gcc acc tgc ctg gac agg aag aca gtg 365
Phe Ser Glu Val Tyr Lys Ala Thr Cys Leu Leu Asp Arg Lys Thr Val
60 65 70

gct ctg aag aag gtg cag atc ttt gag atg atg gac gcc aag gcg agg 413
Ala Leu Lys Lys Val Gln Ile Phe Glu Met Met Asp Ala Lys Ala Arg
75 80 85

cag gac tgt gtc aag gag atc ggc ctc ttg aag caa ctg aac cac cca 461
Gln Asp Cys Val Lys Glu Ile Gly Leu Leu Lys Gln Leu Asn His Pro
90 95 100

aat atc atc aag tat ttg gac tcg ttt atc gaa gac aac gag ctg aac 509
Asn Ile Ile Lys Tyr Leu Asp Ser Phe Ile Glu Asp Asn Glu Leu Asn
105 110 115

att gtg ctg gag ttg gct gac gca ggg gac ctc tcg cag atg atc aag 557
Ile Val Leu Glu Leu Ala Asp Ala Gly Asp Leu Ser Gln Met Ile Lys
120 125 130 135

tac ttt aag aag cag aag cgg ctc atc ccg gag agg aca gta tgg aag 605
Tyr Phe Lys Lys Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys
140 145 150

tac ttt gtg cag ctg tgc agc gcc gtg gag cac atg cat tca cgc cgg 653
Tyr Phe Val Gln Leu Cys Ser Ala Val Glu His Met His Ser Arg Arg
155 160 165

gtg atg cac cga gac atc aag cct gcc aac gtg ttc atc aca gcc acg 701
Val Met His Arg Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr
170 175 180

ggc gtc gtg aag ctc ggt gac ctt ggt ctg ggc cgc ttc ttc agc tct 749
Gly Val Val Lys Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser
185 190 195

gag acc acc gca gcc cac tcc cta gtg ggg acg ccc tac tac atg tca 797
Glu Thr Thr Ala Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser
200 205 210 215

ccg gag agg atc cat gag aac ggc tac aac ttc aag tcc gac atc tgg 845
Pro Glu Arg Ile His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp
220 225 230

tcc ttg ggc tgt ctg ctg tac gag atg gca gcc ctc cag agc ccc ttc 893
Ser Leu Gly Cys Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe
235 240 245

tat gga gat aag atg aat ctc ttc tcc ctg tgc cag aag atc gag cag 941
Tyr Gly Asp Lys Met Asn Leu Phe Ser Leu Cys Gln Lys Ile Glu Gln
250 255 260

tgt gac tac ccc cca ctc ccc ggg gag cac tac tcc gag aag tta cga 989
Cys Asp Tyr Pro Pro Leu Pro Gly Glu His Tyr Ser Glu Lys Leu Arg
265 270 275

gaa ctg gtc agc atg tgc atc tgc cct gac ccc cac cag aga cct gac 1037
110/546

Glu Leu Val Ser Met Cys Ile Cys Pro Asp Pro His Gln Arg Pro Asp
280 285 290 295

atc gga tac gtg cac cag gtg gcc aag cag atg cac atc tgg atg tcc 1085
Ile Gly Tyr Val His Gln Val Ala Lys Gln Met His Ile Trp Met Ser
300 305 310

agc acc tgagcggttga tgcacccgtgc ctatcaaag ccagcaccac ttgccttac 1141

Ser Thr

ttgagtcgtc ttctcttgcgatggccacctt ggttagccatgg aacagctaaaccacagggt 1201

tcagcagggtt ccccaaaagg ctgcccgacc ttacagcaga tgctgaaggc agagcagctg 1261

agggaggggc gctggccaca tgtcactgtatggcataatcc caaagtccctt tctttatact 1321

gttgtggaca atctcagctg ggtcaataag ggcagggtgt tcagcgagcc acggcagccc 1381

cctgtatctg gattgtaatg tgaatcttta ggtaattcc tccagtgacc tgtcaaggct 1441

tatgctaaca ggagacttgc aggagaccgt gtgatttgc tagtgaggct ttgaaaatgg 1501

tttgttccgg gttcagttta gttcttgta tctttcaat caagctgtgt gcttaattta 1561

ctctgttgta aaggataaaa gtggaaatca tttttt 1597

<210> 41

<211> 371

<212> PRT

<213> Homo sapiens

<400> 41

Met Ser His Glu Lys Ser Phe Leu Val Ser Gly Asp Asn Tyr Pro Pro
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Pro Asn Pro Gly Tyr Pro Gly Gly Pro Gln Pro Pro Met Pro Pro Tyr
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Ala Gln Pro Pro Tyr Pro Gly Ala Pro Tyr Pro Gln Pro Pro Phe Gln
35 40 45

Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro Ser Pro Tyr
50 55 60

Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro
65 70 75 80

Gln Gly Pro Tyr Pro Gln Glu Gly Tyr Pro Gln Gly Pro Tyr Pro Gln
85 90 95

Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Ser Pro Phe Pro Pro Asn
100 105 110

Pro Tyr Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro Asp Ser Pro
115 120 125

Gln His Gly Asn Tyr Gln Glu Glu Gly Pro Pro Ser Tyr Tyr Asp Asn

130

135

140

Gln Asp Phe Pro Ala Thr Asn Trp Asp Asp Lys Ser Ile Arg Gln Ala

145

150

155

160

Phe Ile Arg Lys Val Phe Leu Val Leu Thr Leu Gln Leu Ser Val Thr

165

170

175

Leu Ser Thr Val Ser Val Phe Thr Phe Val Ala Glu Val Lys Gly Phe

180

185

190

Val Arg Glu Asn Val Trp Thr Tyr Tyr Val Ser Tyr Ala Val Phe Phe

195

200

205

Ile Ser Leu Ile Val Leu Ser Cys Cys Gly Asp Phe Arg Arg Lys His

210

215

220

Pro Trp Asn Leu Val Ala Leu Ser Val Leu Thr Ala Ser Leu Ser Tyr

225

230

235

240

Met Val Gly Met Ile Ala Ser Phe Tyr Asn Thr Glu Ala Val Ile Met

245

250

255

Ala Val Gly Ile Thr Thr Ala Val Cys Phe Thr Val Val Ile Phe Ser

260

265

270

Met Gln Thr Arg Tyr Asp Phe Thr Ser Cys Met Gly Val Leu Leu Val

275

280

285

Ser Met Val Val Leu Phe Ile Phe Ala Ile Leu Cys Ile Phe Ile Arg
290 295 300

Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser Leu Gly Ala Leu Leu Phe
305 310 315 320

Thr Cys Phe Leu Ala Val Asp Thr Gln Leu Leu Leu Gly Asn Lys Gln
325 330 335

Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe Ala Ala Leu Asn Leu Tyr
340 345 350

Thr Asp Ile Ile Asn Ile Phe Leu Tyr Ile Leu Thr Ile Ile Gly Arg
355 360 365

Ala Lys Glu

370

<210> 42

<211> 1781

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91)..(1203)

<400> 42

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ccaccggggc ggaccgcgga acccgaggcc atg tcc cat gaa aag agt ttt ttg 114
Met Ser His Glu Lys Ser Phe Leu

1 5

gtg tct ggg gac aac tat cct ccc ccc aac cct gga tat ccg ggg ggg 162
Val Ser Gly Asp Asn Tyr Pro Pro Pro Asn Pro Gly Tyr Pro Gly Gly

10 15 20

ccc cag cca ccc atg ccc ccc tat gct cag cct ccc tac cct ggg gcc 210
Pro Gln Pro Pro Met Pro Pro Tyr Ala Gln Pro Pro Tyr Pro Gly Ala
25 30 35 40

cct tac cca cag ccc cct ttc cag ccc tcc ccc tac ggt cag cca ggg 258
Pro Tyr Pro Gln Pro Pro Phe Gln Pro Ser Pro Tyr Gly Gln Pro Gly
45 50 55

tac ccc cat ggc ccc agc ccc tac ccc caa ggg ggc tac cca cag ggt 306
Tyr Pro His Gly Pro Ser Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly
60 65 70

ccc tac ccc caa ggg ggc tac cca cag ggc ccc tac cca caa gag ggc 354
Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Glu Gly
75 80 85

tac cca cag ggc ccc tac ccc caa ggg ggc tac ccc cag ggg cca tat 402
Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr
90 95 100

ccc cag agc ccc ttc ccc ccc aac ccc tat gga cag cca cag gtc ttc 450
Pro Gln Ser Pro Phe Pro Pro Asn Pro Tyr Gly Gln Pro Gln Val Phe
105 110 115 120

cca gga caa gac cct gac tca ccc cag cat gga aac tac cag gag gag 498
Pro Gly Gln Asp Pro Asp Ser Pro Gln His Gly Asn Tyr Gln Glu Glu
125 130 135

ggt ccc cca tcc tac tat gac aac cag gac ttc cct gcc acc aac tgg 546
Gly Pro Pro Ser Tyr Tyr Asp Asn Gln Asp Phe Pro Ala Thr Asn Trp
140 145 150

gat gac aag agc atc cga cag gcc ttc atc cgc aag gtg ttc cta gtg 594
Asp Asp Lys Ser Ile Arg Gln Ala Phe Ile Arg Lys Val Phe Leu Val
155 160 165

ctg acc ttg cag ctg tcg gtg acc ctg acg gtg tct gtg ttc act 642
Leu Thr Leu Gln Leu Ser Val Thr Leu Ser Thr Val Ser Val Phe Thr
170 175 180

ttt gtt gcg gag gtg aag ggc ttt gtc cgg gag aat gtc tgg acc tac 690
Phe Val Ala Glu Val Lys Gly Phe Val Arg Glu Asn Val Trp Thr Tyr
185 190 195 200

tat gtc tcc tat gct gtc ttc ttc atc tct ctc atc gtc ctc agc tgt 738
Tyr Val Ser Tyr Ala Val Phe Phe Ile Ser Leu Ile Val Leu Ser Cys
205 210 215

tgt ggg gac ttc cgg cga aag cac ccc tgg aac ctt gtt gca ctg tcg 786
Cys Gly Asp Phe Arg Arg Lys His Pro Trp Asn Leu Val Ala Leu Ser
220 225 230

gtc ctg acc gcc agc ctg tcg tac atg gtg ggg atg atc gcc agc ttc 834
Val Leu Thr Ala Ser Leu Ser Tyr Met Val Gly Met Ile Ala Ser Phe
235 240 245

882
tat aac acc gag gca gtc atc atg gcc gtg ggc atc acc aca gcc gtc
Tyr Asn Thr Glu Ala Val Ile Met Ala Val Gly Ile Thr Thr Ala Val
250 255 260

930
tgc ttc acc gtc gtc atc ttc tcc atg cag acc cgc tac gac ttc acc
Cys Phe Thr Val Val Ile Phe Ser Met Gln Thr Arg Tyr Asp Phe Thr
265 270 275 280

978
tca tgc atg ggc gtg ctc ctg gtg agc atg gtg gtg ctc ttc atc ttc
Ser Cys Met Gly Val Leu Leu Val Ser Met Val Val Leu Phe Ile Phe
285 290 295

1026
gcc att ctc tgc atc ttc atc cgg aac cgc atc ctg gag atc gtg tac
Ala Ile Leu Cys Ile Phe Ile Arg Asn Arg Ile Leu Glu Ile Val Tyr
300 305 310

1074
gcc tca ctg ggc gct ctg ctc acc tgc ttc ctc gca gtg gac acc
Ala Ser Leu Gly Ala Leu Leu Phe Thr Cys Phe Leu Ala Val Asp Thr
315 320 325

1122
cag ctg ctg ctg ggg aac aag cag ctg tcc ctg agc cca gaa gag tat

Gln Leu Leu Leu Gly Asn Lys Gln Leu Ser Leu Ser Pro Glu Glu Tyr
330 335 340

gtg ttt gct gcg ctg aac ctg tac aca gac atc atc aac atc ttc ctg 1170
Val Phe Ala Ala Leu Asn Leu Tyr Thr Asp Ile Ile Asn Ile Phe Leu
345 350 360

tac atc ctc acc atc att ggc cgc gcc aag gag tagccgagct ccagctcgct 1223
Tyr Ile Leu Thr Ile Ile Gly Arg Ala Lys Glu
365 370

gtgccccgtc aggtggcacg gctggcctgg accctgcccc tggcacggca gtgccagctg 1283

tacttccccct ctctcttgtc cccaggcaca gccttagggaa aaggatgcct ctctccaacc 1343

ctccctgtatg tacactgcag atacttccat ttggacccgc tgtggccaca gcatggcccc 1403

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tactcatgt tgcatgagcc ctgtctgcca gcccacccca gggactgggg gcagcaccag 1523

gtcccgggga gagggattga gccaagaggt gagggtgcac gtctccctc ctgtcccagc 1583

tcccccagct ggcgttagagc accccctcccc tccccccac cccctggag tgctgccctc 1643

tggggacatg cggagtgggg gtcttatccc tgtgctgagc cctgagggca gagaggatgg 1703

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1781

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<210> 43

〈211〉 393

<212> PRT

<213> Homo sapiens

<400> 43

<400> 43 Met Ser Asp Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala
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1 5 10

Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro
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Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu
 50 55 60

Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met
 100 105 110

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg
115 120 125

Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln
130 135 140

Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala
145 150 155 160

Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala
165 170 175

Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val
180 185 190

Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu
195 200 205

Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser
210 215 220

Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr
225 230 235 240

His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly
245 250 255

Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly

260

265

270

Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala

275

280

285

Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr

290

295

300

Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Gln Ala Asn

305

310

315

320

Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu

325

330

335

Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly

340

345

350

His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala

355

360

365

Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu

370

375

380

Leu Val Pro Gly Pro Glu Lys Glu Asn

385

390

<210> 44

<211> 2396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)..(1228)

<400> 44

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 Met Ser Asp

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gag aga gag gta gcc gag gca gcg acc ggg gaa gac gcc tct tcg ccg 106
 Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro

5

10

15

cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc 154
 Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser

20

25

35

gaa ggg gcc gcc gcc gcc gac ccg cca ctg ctg cgc tgc cta 202
 Glu Gly Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu

40

45

50

gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg 250
 Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg

55

60

65

ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg 298

Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu
70 75 80

cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg 346
Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu
85 90 95

taa gac cgt ctc ccc cct ctg cct gtc act ccg ggc atg gag ggc gcg 394
Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala
100 105 110 115

ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga 442
Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly
120 125 130

gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg 490
Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val
135 140 145

act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt 538
Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe
150 155 160

gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc 586
Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val
165 170 175

ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac 634
Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His

180

185

190

195

atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca 682
Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr

200

205

210

gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag 730
Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu

215

220

225

gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act 778
Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr

230

235

240

gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att 826
Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile

245

250

255

gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc 874
Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu
260 265 270 275

ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg 922
Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu

280

285

290

acg ggc ccc aaa cggt aac ctg atg gcc ctg gcc cgg aca tgg tgg aat 970
Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn

295

300

305

cag ttc agc gtg aca gct ctg cag ctg cag gcc aac cgg gct gtg 1018
Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val
310 315 320

tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt 1066
Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser
325 330 335

ggc gtg gtc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag 1114
Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys
340 345 350 355

ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg 1162
Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met
360 365 370

aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca 1210
Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro
375 380 385

ggg cca gag aag gag aac tagggcaagt ggctgtgaga cccttagagac 1258
Gly Pro Glu Lys Glu Asn
390

cagcgaagg aagaaggtaagg aagctacgtt ctgttgccca ccagacttgc attcagcct 1318

ctgtcataat gctctgcct ccctcccccg aagttctctg tggtgatgac cgctctcccc 1378

tgcctcccgatgtctggg 1438
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ccctgccaag ggcacaggga gggcagagg gaggccgct gcttcctgcc cccaccctt 1498

ccccgggcct gctgtctgc ttgtgtccca aggttagccaa gtcccccctg ttgtgttcca 1558

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cttccctcagc ctgcagata tgtgtggcat ttactagccaa gagctctgaa aggcaagtgc 1978

gtctgtttct tgtactggga ccaaagtaaa aatccaaagca cattccctt gcagttggg 2038

gaggccctac tgccttcata aagcagagag gcagcttatac aaactcagcc caaaactctg 2098

tttacatggg tggggagatg gagcaggaa gtacagatg ggtatggtcag gacctggcc 2158

attgcaacca aatggggac ttccctggta gggaggtcac tccctctact cactgagcta 2218

ggattaggga gggttattgc cccaaaccatt gcaatgggag gtggagggac aggctcagcc 2278

tcctcatgt ctaaatgagg cctaaatgtg tgaagtgcga tttctgcctt tgtgtacccc 2338

accaccccat taccacagct gcctttgtgt gtttgtgtca ataaaaagcc aaaccctg 2396

<210> 45

<211> 393

<212> PRT

<213> Homo sapiens

<400> 45

Met Ser Asp Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala
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Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro
20 25 30

Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu
35 40 45

Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu
50 55 60

Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr
65 70 75 80

Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg
85 90 95

Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met

100

105

110

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg

115

120

125

Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln

130

135

140

Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala

145

150

155

160

Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala

165

170

175

Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val

180

185

190

Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu

195

200

205

Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser

210

215

220

Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr

225

230

235

240

His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly

245

250

255

Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly

260

265

270

Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala

275

280

285

Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr

290

295

300

Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn

305

310

315

320

Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu

325

330

335

Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly

340

345

350

His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala

355

360

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Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu

370

375

380

Leu Val Pro Gly Pro Glu Lys Gln Asn

385

390

<210> 46

<211> 2396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)..(1228)

<400> 46

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Met Ser Asp

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Glu Arg Glu Val Ala Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro

5 10 15

cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc 154
Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser
20 25 30 35

gaa ggg gcc gcc gcc gcc tcg ccg cca ctg ctg cgc tgc cta 202
Glu Gly Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu
40 45 50

gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg 250
Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg

55

60

65

ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg 298
Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu

70

75

80

cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg 346
Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu

85

90

95

tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc ggc 394
Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala

100

105

110

115

ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga 442
Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly

120

125

130

gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg 490
Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val

135

140

145

act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt 538
Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe

150

155

160

gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc 586
Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val

165

170

175

ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac 634
Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His
180 185 190 195

atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca 682
Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr
200 205 210

gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag 730
Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu
215 220 225

gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act 778
Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr
230 235 240

gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att 826
Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile
245 250 255

gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc 874
Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu
260 265 270 275

ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg 922
Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu
280 285 290

acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat 970
Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn
295 300 305

cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg 1018
Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val
310 315 320

tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt 1066
Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser
325 330 335

ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag 1114
Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys
340 345 350 355

ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg 1162
Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met
360 365 370

aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca 1210
Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro
375 380 385

ggg cca gag aag cag aac tagggcaagt ggctgtgaga ccctagagac 1258
Gly Pro Glu Lys Gln Asn
390

cagcgaaggg agaagttggg aagctacgtt ctgttgccca ccagacttgc atttcagcct 1318

cgtcataat gcctcgccct ccctcccccg aagttctctg tggtgatgac cgctctcccc 1378

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ggatttaggga gggttattgc cccaaccatt gcaatggag gtggagggac aggctcagcc 2278

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<210> 47

<211> 138

<212> PRT

<213> Homo sapiens

<400> 47

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Phe Gly Val Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys
20 25 30

Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe
35 40 45

Val Ile Gly Leu Glu Arg Thr Phe Arg Phe Phe Gin Lys His Lys
50 55 60

Met Lys Ala Thr Gly Phe Phe Leu Gly Val Phe Val Val Leu Ile
65 70 75 80

Gly Trp Pro Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu
85 90 95

Leu Phe Arg Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val
100 105 110

Pro Val Leu Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val
115 120 125

Asp Lys Val Gly Glu Ser Asn Asn Met Val
130 135

<210> 48

<211> 2976

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (110)..(523)

<400> 48

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accctgggct tcccgagggtg ctgtcgccgc tgtccccacc actgcagcc atg atc tcc 118
Met Ile Ser

tta acg gac acg cag aaa att gga atg gga tta aca gga ttt gga gtg 166
Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr Gly Phe Gly Val
5 10 15

ttt ttc ctg ttc ttt gga atg att ctc ttt ttt gac aaa gca cta ctg 214
Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys Ala Leu Leu
20 25 30 35

gct att gga aat gtt tta ttt gta gcc ggc ttg gct ttt gta att ggt 262
Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe Val Ile Gly
40 45 50

tta gaa aga aca ttc aga ttc ttc caa aaa cat aaa atg aaa gct 310
Leu Glu Arg Thr Phe Arg Phe Phe Gln Lys His Lys Met Lys Ala
55 60 65

aca ggt ttt ttt ctg ggt ggt gta ttt gta gtc ctt att ggt tgg cct 358
Thr Gly Phe Phe Leu Gly Val Phe Val Val Leu Ile Gly Trp Pro
70 75 80

ttg ata ggc atg atc ttc gaa att tat gga ttt ttt ctc ttg ttc agg 406
Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu Phe Arg
85 90 95

ggc ttc ttt cct gtc gtt ggc ttt att aga aga gtg cca gtc ctt 454
Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val Pro Val Leu
100 105 110 115

gga tcc ctc cta aat tta cct gga att aga tca ttt gta gat aaa gtt 502
Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val Asp Lys Val
120 125 130

gga gaa agc aac aat atg gta taacaacaag tgaatttcaa gactcattt 553
Gly Glu Ser Asn Asn Met Val
135

aaatatttgtt ttatttataa agtcatttga agaatattca gcacaaaatt aaattacatg 613

aaatagcttg taatgttctt tacaggagtt taaaacgtat agcctacaaa gtaccagcag 673

caaatttagca aagaaggagt gaaaacaggc ttctactcaa gtgaactaag aagaagtcag 733

caagcaaact gagagaggtg aaatccatgt taatgtatc taagaaactc ttgaaggcta 793

tttgttgtt tttccacaa tgtgcgaaac tcagccatcc ttagagaact gtggcgctg 853

tttctttct ttttattttg aaggctcagg agcatccata ggcatttgtt ttttagaaat 913

gtccactgca atggcaaaaa tatttccagt tgcaactgtat ctctggaagt gaigcatgaa 973

ttcgattgga ttgtgtcatt ttaaagtatt aaaacccaagg aaaccccaat ttgatgtat 1033

ggattacttt ttttgtaaa catggtaaa ataaaacttc tgtggctt ctgaatctt 1093

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tgtcatgtatg taattttct ttcttcatttc tttttttaa attttagcag tggcttattta 1453

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ttgcgttta ttagacagta ggaaatagct gttttctta gttttacaag atgtgacagc 1813

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aatctgttgtt atttattttac aaacatgtct acaaaaatag attacagctt attttatttt 1993

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gttaatggaa taataagagg ctactgtgt gtcataatgtt cttcaaaaaa gtaataatcct 2233

cacttggaga gtgtcaaata catacttga ggattgactt tatataaggt gccctgtaga 2293

actctgttac acatattttt gaccatatt atttacaatg tcttgcataat tctacccttt 2353

tagagcaaga atagtatctg ctaatgtaa ggacatctgt atttaactcc ttgttagaca 2413

tgaatttcta tcaaatgtt ctgtgcactg taacagagat cccttttc aataatctta 2473

attcaaaagc attatttagac ttgaaagggt ttgataatct cccagtcctt agtaaagatt 2533

gagagaggct ggagcagttt tcagtttaa atgagtcgc agttaataatc aaatgtgagt 2593

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cagccctctg tctgtacaa aaatgtactt tatagagatg gagaaaaagg tctaataacta 2773

catagccctta agtgtttctg tcattgtca agtgttattt ctgtacaga aacatatttg 2833

gaatgtttt ctttccct tataaattgt aattcctgaa atactgctgc tttaaaaagt 2893

cccactgtca gattatatta tctaacaatt gaatattgt aatatacttg tcttacctct 2953

2976

caataaaagg gtactttctt att

<210> 49

<211> 359

<212> PRT

<213> Homo sapiens

<400> 49

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1 5 10 15

His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln
20 25 30

Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val
35 40 45

Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro
50 55 60

Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met
65 70 75 80

Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile
85 90 95

Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser

100 105 110

Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu
115 120 125

His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp
130 135 140

Cys Leu Glu Ile Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg
145 150 155 160

Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His
165 170 175

Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr
180 185 190

Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu
195 200 205

Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro
210 215 220

Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile
225 230 235 240

Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser
245 250 255

Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser
260 265 270

Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe
275 280 285

Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His
290 295 300

Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met
305 310 315 320

Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser
325 330 335

Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser His Thr Leu Ser
340 345 350

Arg Ser Thr Thr His Leu Ile
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<210> 50

<211> 2636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (327).. (1403)

<400> 50

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aacgtggtgg acctatccit gcaccagagg agattaagac tattttggt agcatcccag 180

atatcttga tgtacacact aagataaagg atgatcttga agaccttata gttaaattggg 240

atgagagcaa aagcatttgtt gacatttttc tgaaatattc aaaagatttg gtaaaaacct 300

accctccctt tgtaaacttc tttgaa atg agc aag gaa aca att att aaa tgt 353

Met Ser Lys Glu Thr Ile Ile Lys Cys

1

5

gaa aaa cag aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca 401

Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala

10

15

20

25

aaa cca gaa tgt gga cgg cag agc ctt gtt gaa ctt ctt atc cga cca 449

Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro

30

35

40

gta cag agg tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag 497

Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys

45

50

55

cat aca gct gat gaa aat cca gac aaa agc act tta gaa aaa gct att 545
His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile
60 65 70

gga tca ctg aag gaa gta atg acg cat att aat gag gat aag aga aaa 593
Gly Ser Leu Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys
75 80 85

aca gaa gct caa aag caa att ttt gat gtt gtt tat gaa gta gat gga 641
Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly
90 95 100 105

tgc cca gct aat ctt tta tct tct cac cga agc tta gta cag cgg gtt 689
Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser Leu Val Gln Arg Val
110 115 120

gaa aca att tct cta ggt gag cac ccc tgt gac aga gga gaa caa gta 737
Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Gln Val
125 130 135

act ctc ttc ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac 785
Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile Ala Arg Lys Arg His
140 145 150

aag gtt att ggc act ttt agg agt cct cat ggc caa acc cga ccc cca 833
Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro
155 160 165

gct tct ctt aag cat att cac cta atg cct ctt tct cag att aag aag 881

Ala Ser Leu Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys
170 175 180 185

gta ttg gac ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg 929
Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu
190 195 200

ctt gtg agg cca cca aca gag cag gca aat gtg cta ctc agt ttc cag 977
Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln
205 210 215

atg aca tca gat gaa ctt cca aaa gaa aac tgg cta aag atg ctg tgt 1025
Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys
220 225 230

cga cat gta gct aac acc att tgt aaa gca gat gct gag aat ctt att 1073
Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile
235 240 245

tat act gct gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac 1121
Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp
250 255 260 265

agt aca ttg agt aga gca tca aga gca ata aaa aag act tca aaa aag 1169
Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys
270 275 280

gtt aca aga gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga 1217
Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg

285

290

295

agg gct ctt atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc 1265
Arg Ala Leu Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser

300

305

310

agc aat gat aag cat gta atg agt cgt ctt tct agc aca tca tca tta 1313
Ser Asn Asp Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Leu

315

320

325

gca ggt atc cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa 1361
Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu
330 335 340 345

agg aga agt cat acg tta agt aga tct aca act cat ttg ata 1403
Arg Arg Ser His Thr Leu Ser Arg Ser Thr Thr His Leu Ile
350 355

tgaagcgta ccaaaatctt aaattataga aatgtataga cacctcatac tcaaataaga 1463

aactgactta aatggtactt gtaatttagca ctggtgaaa gctggaaagga agataaataa 1523

cactaaacta tgctatggta ttttctct tgaaagagta aggtttacct gttacatttt 1583

caagtttaatt catgtaaaaa atgatagtga ttttgatgta atttatctt tggtaatc 1643

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tgatagagta aataaatttt atggcggtt gccaaatact gctgtgaatc tatttgtata 1763

gtatccatga atgaatttat ggaaatagat atttgtgcag ctcaatttat gcagagatta 1823

aatgacatca taatactgga tgaaaacttg catagaattc tgattaaata gtgggtctgt 1883

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aagcgtttc aagatctgc atgtggattt taaaagattt gcctcatta acaagaataa 2003

catttaaagg agatgtttc aaaatatttt tgcaaattt gataaggaca gaaagattga 2063

gaaacatgt atattttgc aaaaacaagat gttttagct gtttcagaga gagtacgta 2123

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tatttgaag gataagacca tggaaaattt gtggtaaaga ctgtttgtac cttcatgaa 2243

ataattctga agttgccatc agttttacta atcttcgtt aatgcatac atatgcgcac 2303

gttcaacttt ttattgtggt cttataattt aatgtaaaat tggaaattca tttgcgttt 2363

caaagtgtga tatctticac aatagccttt ttatagtcag taattcagaa taatcaagtt 2423

catatggata aatgcatttt tatttcctat ttcttttaggg agtgctacaa atgtttgtca 2483

cttaaatttc aagtttctgt tttatagtt aactgactat agattgttt ctatgccatg 2543

tatgtgccac ttctgagagt agtaaatgac tctttgctac attttaaaag caattgtatt 2603

agtaagaact ttgtaaataa atacctaataa ccc

2636

<210> 51

<211> 883

<212> PRT

<213> Homo sapiens

<400> 51

Met Ala Glu Asn Ser Val Leu Thr Ser Thr Thr Gly Arg Thr Ser Leu
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Ala Asp Ser Ser Ile Phe Asp Ser Lys Val Thr Glu Ile Ser Lys Glu
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Asn Leu Leu Ile Gly Ser Thr Ser Tyr Val Glu Glu Glu Met Pro Gln
35 40 45

Ile Glu Thr Arg Val Ile Leu Val Gln Glu Ala Gly Lys Gln Glu Glu
50 55 60

Leu Thr Lys Ala Leu Lys Asp Ile Lys Val Gly Phe Val Lys Met Glu
65 70 75 80

Ser Val Glu Glu Phe Glu Gly Leu Asp Ser Pro Glu Phe Glu Asn Val
85 90 95

Phe Val Val Thr Asp Phe Gln Asp Ser Val Phe Asn Asp Leu Tyr Lys
100 105 110

Ala Asp Cys Arg Val Ile Gly Pro Pro Val Val Leu Asn Cys Ser Gln
115 120 125

Lys Gly Glu Pro Leu Pro Phe Ser Cys Arg Pro Leu Tyr Cys Thr Ser
130 135 140

Met Met Asn Leu Val Leu Cys Phe Thr Gly Phe Arg Lys Lys Glu Glu
145 150 155 160

Leu Val Arg Leu Val Thr Leu Val His His Met Gly Gly Val Ile Arg
165 170 175

Lys Asp Phe Asn Ser Lys Val Thr His Leu Val Ala Asn Cys Thr Gln
180 185 190

Gly Glu Lys Phe Arg Val Ala Val Ser Leu Gly Thr Pro Ile Met Lys
195 200 205

Pro Glu Trp Ile Tyr Lys Ala Trp Glu Arg Arg Asn Glu Gln Asp Phe
210 215 220

Tyr Ala Ala Val Asp Asp Phe Arg Asn Glu Phe Lys Val Pro Pro Phe
225 230 235 240

Gln Asp Cys Ile Phe Ser Phe Leu Gly Phe Ser Asp Glu Glu Lys Thr
245 250 255

Asn Met Glu Glu Met Thr Glu Met Gln Gly Gly Lys Tyr Leu Pro Leu

260

265

270

Gly Asp Glu Arg Cys Thr His Leu Val Val Glu Glu Asn Ile Val Lys

275

280

285

Asp Leu Pro Phe Glu Pro Ser Lys Lys Leu Tyr Val Val Lys Gln Glu

290

295

300

Trp Phe Trp Gly Ser Ile Gln Met Asp Ala Arg Ala Gly Glu Thr Met

305

310

315

320

Tyr Leu Tyr Glu Lys Ala Asn Thr Pro Glu Leu Lys Lys Ser Val Ser
325 330 335Met Leu Ser Leu Asn Thr Pro Asn Ser Asn Arg Lys Arg Arg Arg Leu
340 345 350Lys Glu Thr Leu Ala Gln Leu Ser Arg Asp Thr Asp Val Ser Pro Phe
355 360 365Pro Pro Arg Lys Arg Pro Ser Ala Glu His Ser Leu Ser Ile Gly Ser
370 375 380Leu Leu Asp Ile Ser Asn Thr Pro Glu Ser Ser Ile Asn Tyr Gly Asp
385 390 395 400Thr Pro Lys Ser Cys Thr Lys Ser Ser Lys Ser Thr Pro Val Pro
405 410 415

Ser Lys Gln Ser Ala Arg Trp Gln Val Ala Lys Glu Leu Tyr Gln Thr
420 425 430

Glu Ser Asn Tyr Val Asn Ile Leu Ala Thr Ile Ile Gln Leu Phe Gln
435 440 445

Val Pro Leu Glu Glu Gly Gln Arg Gly Gly Pro Ile Leu Ala Pro
450 455 460

Glu Glu Ile Lys Thr Ile Phe Gly Ser Ile Pro Asp Ile Phe Asp Val
465 470 475 480

His Thr Lys Ile Lys Asp Asp Leu Glu Asp Leu Ile Val Asn Trp Asp
485 490 495

Glu Ser Lys Ser Ile Gly Asp Ile Phe Leu Lys Tyr Ser Lys Asp Leu
500 505 510

Val Lys Thr Tyr Pro Pro Phe Val Asn Phe Phe Glu Met Ser Lys Glu
515 520 525

Thr Ile Ile Lys Cys Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu
530 535 540

Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu
545 550 555 560

Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val Ala Leu Leu
565 570 575

Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr
580 585 590

Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met Thr His Ile Asn
595 600 605

Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val
610 615 620

Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser
625 630 635 640

Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp
645 650 655

Arg Gly Glu Gln Val Thr Leu Phe Asn Asp Cys Leu Glu Ile
660 665 670

Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly
675 680 685

Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His Leu Met Pro Leu
690 695 700

Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His
705 710 715 720

Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val

725

730

735

Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp

740

745

750

Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp

755

760

765

Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn

770

775

780

Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys

785

790

795

800

Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro

805

810

815

Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His Gly Ser Val Glu

820

825

830

Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met Ser Arg Leu Ser

835

840

845

Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu

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Ser Thr Thr Gly Arg Thr Ser Leu Ala Asp Ser Ser Ile Phe Asp Ser
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Lys Val Thr Glu Ile Ser Lys Glu Asn Leu Leu Ile Gly Ser Thr Ser
25 30 35 40

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Tyr Val Glu Glu Glu Met Pro Gln Ile Glu Thr Arg Val Ile Leu Val
45 50 55

caa gaa gct gga aaa caa gaa gaa ctt aca aaa gcc tta aag gac att 244
Gln Glu Ala Gly Lys Gln Glu Glu Leu Thr Lys Ala Leu Lys Asp Ile
60 65 70

aaa gtg ggc ttt gta aag atg gag tca gtg gaa gaa ttt gaa ggt ttg 292
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75 80 85

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Asp Ser Pro Glu Phe Glu Asn Val Phe Val Val Thr Asp Phe Gln Asp
90 95 100

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Ser Val Phe Asn Asp Leu Tyr Lys Ala Asp Cys Arg Val Ile Gly Pro
105 110 115 120

cca gtt gta tta aat tgt tca caa aaa gga gag cct ttg cca ttt tca 436
Pro Val Val Leu Asn Cys Ser Gln Lys Gly Glu Pro Leu Pro Phe Ser
125 130 135

tgt cgc ccg ttg tat tgt aca agt atg atg aat cta gta cta tgc ttt 484
Cys Arg Pro Leu Tyr Cys Thr Ser Met Met Asn Leu Val Leu Cys Phe
140 145 150

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Thr Gly Phe Arg Lys Lys Glu Glu Leu Val Arg Leu Val Thr Leu Val
155 160 165

cat cac atg ggt gga gtt att cga aaa gac ttt aat tca aaa gtt aca 580
His His Met Gly Gly Val Ile Arg Lys Asp Phe Asn Ser Lys Val Thr
170 175 180

cat ttg gtg gca aat tgt aca caa gga gaa aaa ttc agg gtt gct gtg 628
His Leu Val Ala Asn Cys Thr Gln Gly Glu Lys Phe Arg Val Ala Val
185 190 195 200

agt cta ggt act cca att atg aag cca gaa tgg att tat aaa gct tgg 676
Ser Leu Gly Thr Pro Ile Met Lys Pro Glu Trp Ile Tyr Lys Ala Trp
205 210 215

gaa agg cggt aat gaa cag gat ttc tat gca gca gtt gat gac ttt aga 724
Glu Arg Arg Asn Glu Gln Asp Phe Tyr Ala Ala Val Asp Asp Phe Arg
220 225 230

aat gaa ttt aaa gtt cct cca ttt caa gat tgt att ttt agt ttc ctg 772
Asn Glu Phe Lys Val Pro Pro Phe Gln Asp Cys Ile Phe Ser Phe Leu
235 240 245

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Gly Phe Ser Asp Glu Glu Lys Thr Asn Met Glu Glu Met Thr Glu Met
250 255 260

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Gln Gly Gly Lys Tyr Leu Pro Leu Gly Asp Glu Arg Cys Thr His Leu
265 270 275 280

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Val Val Glu Glu Asn Ile Val Lys Asp Leu Pro Phe Glu Pro Ser Lys
285 290 295

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300 305 310

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315 320 325

cct gag ctc aag aaa tca gtg tca atg ctt tct cta aat acc cct aac 1060
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330 335 340

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365 370 375

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380 385 390

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475

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Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg
555 560 565

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570 575 580

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620 625 630

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635 640 645

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650 655 660

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Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu Val Arg
715 720 725

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Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser
730 735 740

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765 770 775

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780 785 790

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795 800 805

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Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp
825 830 835 840

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Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile
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Cys Lys Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys
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Ile Asp Gly Glu Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln
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His Met Pro Ile Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn
165 170 175

Met Thr Asp Val Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys
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195 200 205

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Ala Leu Gln Asn Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu
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Lys Cys Glu Leu Phe Leu Leu Met Leu Ser Val Ile Thr Met Trp
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Ala Ile Gly Tyr Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys
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Phe Leu Val Gly Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu

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350

Leu Ser Ser Val Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe

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360

365

Pro Asp Leu Ala Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile

370

375

380

Val Ala Phe Leu Tyr Phe Phe Tyr Lys Thr Trp Ala Thr Asp Pro Gly

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420

425

430

Ile Arg Lys Pro Leu Arg Ser Leu His Cys His Val Cys Asn Cys Cys

435

440

445

Val Ala Arg Tyr Asp Gln His Cys Leu Trp Thr Gly Arg Cys Ile Gly

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460

Phe Gly Asn His His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met

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475

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Val Cys Gly Trp Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His
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Ile Val Ala Cys Ser Pro Trp Val Leu Tyr Ile Leu Met Leu Ala Thr
515 520 525

Phe His Phe Ser Trp Ser Thr Phe Leu Leu Asn Gln Leu Phe Gln
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Ile Ala Phe Leu Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys
545 550 555 560

Gln Ser Lys His Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr
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 Met Glu Gly Pro

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 Gly Leu Gly Ser Gln Cys Arg Asn His Ser His Gly Pro His Pro Pro
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 Gly Phe Gly Arg Tyr Gly Ile Cys Ala His Glu Asn Lys Glu Leu Ala
 25 30 35

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Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Ser
70 75 80

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Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp Leu Val Lys Phe
85 90 95 100

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Tyr Ile Ser Lys Gly Ala Val Val Asp Gln Leu Gly Gly Asp Leu Asn
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Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His Leu Pro Met Val
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Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu Ile Asp Gly Glu
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Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln His Met Pro Ile
150 155 160

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Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn Met Thr Asp Val
165 170 175 180

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Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser Leu Asn Val Val			
200	205	210	
gat aaa ata cac caa aac act cca ctt cac tgg gca gtt gca gca gga	787		
Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala Val Ala Ala Gly			
215	220	225	
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Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu Ala Lys Met Arg			
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295 300 305

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325 330 335 340

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345 350 355

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Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile Val Ala Phe Leu
375 380 385

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390 395 400

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His	Tyr	Tyr	Ile	Phe	Phe	Leu	Phe	Phe	Leu	Ser	Met	Val	Cys	Gly	Trp	
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																475
																480
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Ile	Ile	Tyr	Gly	Ser	Phe	Ile	Tyr	Leu	Ser	Ser	His	Cys	Ala	Thr	Thr	
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																490
																495
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Phe	Lys	Glu	Asp	Gly	Leu	Trp	Thr	Tyr	Leu	Asn	Gln	Ile	Val	Ala	Cys	
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																510
																515
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Ser	Pro	Trp	Val	Leu	Tyr	Ile	Leu	Met	Leu	Ala	Thr	Phe	His	Phe	Ser	

tgg tca aca ttt tta tta tta aat caa ctc ttt cag att gcc ttt ctg	520	525	530	1747
Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln Ile Ala Phe Leu				
	535	540	545	
ggc ctg acc tcc cat gag aga atc agc ctg cag aag cag agc aag cat				1795
Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys Gln Ser Lys His				
	550	555	560	
atg aaa cag acg ttg tcc ctc agg aag aca cca tac aat ctt gga ttc				1843
Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr Asn Leu Gly Phe				
	565	570	575	580
atg cag aac ctg gca gat ttc ttt cag tgt ggc tgc ttt ggc ttg gtg				1891
Met Gln Asn Leu Ala Asp Phe Phe Gln Cys Gly Cys Phe Gly Leu Val				
	585	590	595	
aag ccc tgt gtg gta gat tgg aca tca cag tac acc atg gtc ttt cac				1939
Lys Pro Cys Val Val Asp Trp Thr Ser Gln Tyr Thr Met Val Phe His				
	600	605	610	
cca gcc agg gag aag gtt ctt cgc tca gta tgaagaaaaa caacccaaaa				1989
Pro Ala Arg Glu Lys Val Leu Arg Ser Val				
	615	620		
ctctcaatct gatttgtttt tgtttatgtc gatgccctgt agtttgaaag tgaagtaaaag				2049
atttagaatt cacciaagtc caaaggaaaa cacgtggttt ttaaagccat taggtaaaaa				2109

aagttctcaa taaaggcatt acaatttttt aggttagaa agatggactt ttctgataaa 2169

tcttggcaga catctaaaaa aaaaaccata ttttcacaa gaaaatgcaa gttactttt 2229

ttggaaataa tactcactga ttatggataa aatggaatat tttcagatac tatattggct 2289

gtttcaaaat agtactattc tttaaacttg taattttgc taagtttattt gtcttggtt 2349

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aaaaaaatttt ttttgt 2426

<210> 55

<211> 257

<212> PRT

<213> Homo sapiens

<400> 55

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15

Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe

20

25

30

Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro

35

40

45

Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala Val Leu

50 55 60

Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe Ala Leu

65 70 75 80

Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr Ile Gly

85 90 95

Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr Ser Arg

100 105 110

Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly Ala Gly

115 120 125

Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser Thr Gly

130 135 140

Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser Leu Gln

145 150 155 160

His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro Gly Gly

165 170 175

Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu Ala Leu

180 185 190

Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile Leu Ala

195 200 205

Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val Ala Tyr
210 215 220

Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys Leu Leu
225 230 235 240

Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala Thr Asp
245 250 255

Gly

<210> 56

<211> 1520

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (10)..(780)

<400> 56

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Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu

1 5 10

atc atg cag ttg ggt tcg gtg ctg ctc aca cgc tgc ccc ttt tgg ggc 99

Ile Met Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly

15

20

25

30

tgc ttc agc cag ctc atg ctg tac gct gag agg gct gag gca cgc cgg 147

Cys Phe Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg

35

40

45

aag ccc gac atc cca gtg cct tac ctg tat ttc gac atg ggg gca gcc 195

Lys Pro Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala

50

55

60

gtg ctg tgc gct agt ttc atg tcc ttt ggc gtg aag cgg cgc tgg ttc 243

Val Leu Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe

65

70

75

gcg ctg ggg gcc gca ctc caa ttg gcc att agc acc tac gcc gcc tac 291

Ala Leu Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr

80

85

90

atc ggg ggc tac gtc cac tac ggg gac tgg ctg aag gtc cgt atg tac 339

Ile Gly Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr

95

100

105

110

tcg cgc aca gtt gcc atc atc ggc ggc ttt ctt gtg ttg gcc agc ggt 387

Ser Arg Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly

115

120

125

gct ggg gag ctg tac cgc cgg aaa cct cgc agc cgc tcc ctg cag tcc 435

Ala Gly Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser

130 135 140

acc ggc cag gtg ttc ctg ggt atc tac ctc atc tgt gtg gcc tac tca 483
Thr Gly Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser

145 150 155

ctg cag cac agc aag gag gac cgg ctg gcg tat ctg aac cat ctc cca 531
Leu Gln His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro

160 165 170

gga ggg gag ctg atg atc cag ctg ttc ttc gtg ctg tat ggc atc ctg 579
Gly Gly Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu
175 180 185 190

gcc ctg gcc ttt ctg tca ggc tac tac gtg acc ctc gct gcc cag atc 627
Ala Leu Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile
195 200 205

ctg gct gta ctg ctg ccc cct gtc atg ctg ctc att gat ggc aat gtt 675
Leu Ala Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val
210 215 220

gct tac tgg cac aac acg cgg cgt gtt gag ttc tgg aac cag atg aag 723
Ala Tyr Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys
225 230 235

ctc ctt gga gag agt gtg ggc atc ttc gga act gct gtc atc ctg gcc 771
Leu Leu Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala
240 245 250

act gat ggc tgagtttat ggcaagaggc tgagatggc acagggagcc

820

Thr Asp Gly

255

actgagggtc accctgcctt cctccttgct ggcccagctg ctgtttattt atgtttttg 880

gtctgtttgt ttgatctttt gctttttaa aattgttttt tgcatattaag aggccagctca 940

tttgtccaaa tttctggct cagcgcttgg gagggcagga gccctggcac taatgctgta 1000

cagggtttttt tcctgttagg agagctgagg ccagctgccc actgagtcctc ctgtccctga 1060

gaagggagta tggcagggt gggatgcggc tactgagagt gggagagtgg gagacagagg 1120

aaggaagatg gagattggaa gtgagcaaattt gtgaaaaattt cctctttgaa cctggcagat 1180

gcagctaggc tctgcagtgc tttttggaga ctgtgagagg gagtgtgtgtt ttgtacacat 1240

gtggatcagg cccaggaagg gcacagggc tgagcactac agaagtcaca tggttctca 1300

gggtatgcc a gggcagaaa cagtaccggc tctctgtcac tcacctttag agtagagcag 1360

accctttctt gctctggct gtgaagggtt ggagcaggca gtggccagct ttgccttcc 1420

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1520

<210> 57

<211> 107

<212> PRT

<213> Homo sapiens

<400> 57

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Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys Asp Lys
20 25 30

Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln Val Glu
35 40 45

Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu Arg Phe
50 55 60

Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp Ser Ile
65 70 75 80

Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met Arg His
85 90 95

Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val
100 105

<210> 58

<211> 1496

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (9)..(329)

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atc cag gtt ggg gag cat gcc aac aac tac cct gag att gct gca aaa 98
 Ile Gln Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys
 15 20 25 30

gat aag ctg acg gag cta cag ctc cgc gcc cgc cag ttg ctt gat gag 146
 Asp Lys Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln
 35 40 45

gtg gaa cag att cag aag gag cag gat tac caa agg tat cgt gaa gag 194
 Val Glu Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu
 50 55 60

cgc ttc cga ctg acg agc gag agc acc aac cag agg gtc cta tgg tgg 242
 Arg Phe Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp
 65 70 75

tcc att gct cag act gtc atc ctc atc ctc act ggc atc tgg cag aig 290
 Ser Ile Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met
 80 85 90

cgt cac ctc aag agc ttc ttt gag gcc aag aag ctg gtg tagtgccctc 339
 Arg His Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val
 95 100 105

tttgtatgac ctttccttt tacctcattt atttggtaact ttccccacac agtcctttat 399

ccacacctggat ttttagggaa aaaaaatgaa aaagaataag tcacatttgtt tccatggcca 459

caaaccattc agatcagccca ctgtcgacc ctggttctta aggacacatg acattagtc 519

aatctttcaa aatcttgtct tagggcttgtt gaggaatcag aactaaccctt ggactcagtc 579

ctgtttttt tgccctcgagt gattttcctc ttttttac taaaataagca aatgaaaact 639

ctctccatta ccttctgcctt tctttttgtc cacttacgca gtaggtgact ggcatgtgcc 699

acagagcagg ccctgcctca ctgtctgctg gtcagttctg gtttcaactt atggctttgt 759

gaatgtaaat aaggggcagg tcttggccct agaggattga gatgttttc tataatcttag 819

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gcagagttct ttggatacc tgctttcat cccacaggc cttagagtca gaggttaagg 1359

agcaacagag ctagaatggg gcaatgcact cttaccctcc ttctcaactt ttatctaagg 1419

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1496

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<210> 59

<211> 272

〈212〉 PRT

<213> Homo sapiens

<400> 59

<400> 39 Met Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly
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15

Pro Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp
20 25 30

Val Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met
35 40 45

Met Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly
50 55 60

Ile Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln
65 70 75 80

Gly Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr
85 90 95

Glu Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr
100 105 110

Thr Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys
115 120 125

Val Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg
130 135 140

Glu Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu
145 150 155 160

His Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro

165

170

175

Ser Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val

180

185

190

Leu Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr

195

200

205

Tyr Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu

210

215

220

Met His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln

225

230

235

240

Tyr Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu

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250

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Arg Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu

260

265

270

<210> 60

<211> 1916

<212> DNA

<213> Homo sapiens

<220>

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<222> (117)..(932)

<400> 60

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gccgcccggcgtcgcc ttattccttg tggcctctgc gggtcctgcc tcagcc atg 119

Met

1

atg atc cac ggc ttc cag agc agc cac cgg gat ttc tgc ttc ggg ccc 167

Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly Pro

5

10

15

tgg aag ctg acg gcg tcc aag acc cac atc atg aag tcg gcg gat gtg 215

Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp Val

20

25

30

gag aaa tta gcc gat gaa tta cat atg cca tct ctc cct gaa atg atg 263

Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met Met

35

40

45

ttt gga gac aac gtt tta aga atc cag cat ggg tct ggc ttt gga att 311

Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly Ile

50

55

60

65

gag ttc aat gct aca gat gcg tta aga tgt gta aac aac tac caa gga 359

Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln Gly

70

75

80

atg ctt aaa gtg gcc tgt gct gaa gag tgg caa gaa agc agg acg gag 407

Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr Glu

85

90

95

ggt gaa cac tcc aaa gag gtt att aaa cca tat gat tgg acc tat aca 455

Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr Thr

100

105

110

aca gat tat aag gga acc tta ctt gga gaa tct ctt aag tta aag gtt 503

Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys Val

115

120

125

gta cct aca aca gat cat ata gat aca gaa aaa ttg aaa gcc aga gaa 551

Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg Glu

130

135

140

145

cag att aag ttt ttt gaa gaa gtt ctc ctt ttt gag gat gaa ctt cat 599

Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu His

150

155

160

gat cat gga gtt tca agc ctg agt gtg aag att aga gta atg cct tct 647

Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro Ser

165

170

175

agc ttt ttc ctg ctg ttg cgg ttt ttc ttg aga att gat ggg gtg ctt 695

Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val Leu

180

185

190

atc aga atg aat gac acg aga ctt tac cat gag gct gac aag acc tac 743

Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr Tyr

195

200

205

atg tia cga gaa tat acg tca cga gaa agc aaa att tct agt ttg atg 791
 Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu Met

210

215

220

225

cat gtt cca cct tcc ctc ttc acg gaa cct aat gaa ata tcc cag tat 839
 His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln Tyr

230

235

240

tta cca ata aag gaa gca gtt tgt gag aag cta ata ttt cca gaa aga 887
 Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu Arg
 245 250 255

att gat cct aac cca gca gac tca caa aaa agt aca caa gtg gaa 932
 Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu
 260 265 270

taaaaatgtga tacaaacatat actcaactatg gaatctgact ggacaccctg gctatttgta 992

aggggttatt tttattatga gaattaattg ccttgtttat gtacagattt tctgttagcct 1052

taaaggaaaa aaaaataaaag atcggtacag gcagggttca ctcaactgct atttgtactg 1112

tctgtcttca cattcatatt ccagatttat attttctgga gttaaatttg gatgatttct 1172

aaattatcac aaagtggac ctcagcagta gtgtatgtg tgtctcatga gcagttagca 1232

cagtctgcat tcatcatgaa acactatctt ctaccaggag gaggttaatg taaatcacca 1292

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01- 3-26; 7:51PM; 平木国际待事所

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1916
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<210> 61

<211> 219

<212> PRT

<213> Homo sapiens

<400> 61

Met Asn Arg Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser

1

5

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Leu Thr Asp Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp

20

25

30

Lys Lys Ile Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln

Lys Lys Ile Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln

35

40

45

Ile Lys Lys Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys

Ile Lys Lys Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys

50

55

60

Ala Leu Arg Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp

Ala Leu Arg Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp

65

70

75

80

Asn Leu Ala Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile

Asn Leu Ala Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile

85

90

95

Gln Ser Leu Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly

Gln Ser Leu Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly

100

105

110

Val Lys Glu Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile

Val Lys Glu Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile

115

120

125

Glu Asp Leu Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu

Glu Asp Leu Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu

130

135

140

Ile Gln Glu Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu

Ile Gln Glu Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu

145

150

155

160

Asp Asp Leu Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala

165

170

175

Asp Glu Asp Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile

180

185

190

Pro Glu Gly Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val

195

200

205

Asp Glu Phe Gly Leu Pro Gln Ile Pro Ala Ser

210

215

<210> 62

<211> 1362

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (49)..(705)

<400> 62

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Met Asn Arg

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Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser Leu Thr Asp

5

10

15

tgc att ggc acg gtg gac agt aga gca gaa tcc att gac aag aag att 153

Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp Lys Lys Ile

20

25

30

35

tct cga ttg gat gct gag cta gtg aag tat aag gat cag atc aag aag 201

Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln Ile Lys Lys

40

45

50

atg aga gag ggt cct gca aag aat atg gtc aag cag aaa gcc ttg cga 249

Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys Ala Leu Arg

55

60

65

gtt tta aag caa aag agg atg tat gag cag cag cg gac aat ctt gcc 297

Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp Asn Leu Ala

70

75

80

caa cag tca ttc aac atg gaa caa gcc aat tat acc atc cag tct ttg 345

Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile Gln Ser Leu

85

90

95

aag gac acc aag acc acg gtt gat gct atg aaa ctg gga gta aag gaa 393

Lys Asp Thr Lys Thr Val Asp Ala Met Lys Leu Gly Val Lys Glu

100

105

110

115

atg aag aag gca tac aag caa gtg aag atc gac cag att gag gat tta 441

Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile Glu Asp Leu

120

125

130

caa gac cag cta gag gat atg atg gaa gat gca aat gaa atc caa gaa 489

Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu Ile Gln Glu

135

140

145

gca ctg agt cgc agt tat ggc acc cca gaa ctg gat gaa gat gat tta 537

Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu Asp Asp Leu

150

155

160

gaa gca gag ttg gat gca cta ggt gat gag ctt ctg gct gat gaa gac 585

Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala Asp Glu Asp

165

170

175

agt tct tat ttg gat gag gca gca tct gca cct gca att cca gaa ggt 633

Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile Pro Glu Gly

180

185

190

195

gtt ccc act gat aca aaa aac aag gat gga gtt ctg gtg gat gaa ttt 681

Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val Asp Glu Phe

200

205

210

gga ttg cca cag atc cct gct tca tagatttgca tcattcaagc atatcttgta 735

Gly Leu Pro Gln Ile Pro Ala Ser

215

aaacaaacac atattatggg actaggaaat atttatctt ccaaatttgc cataacagat 795

ttaggtttctt ttcctttctt tgaaggaaag tttaattaca ttgctttttt attttttcca 855

ttaagagact cattgcttgg gaaatgcctt ctgcgtacta aaatttgatt cctttttttt 915

cttatgaaaa acgaactcag tttaaaagta ttttagctc gtatgacttg ttttcattca 975

ttaataataa tttgaaataa aactaaggaa atggaatctt aaaagtctat gacagtgtaa 1035

ctctacagtc tcaaaatgac ctgataaatt gataagacaa agatgagatt attggggctg 1095

ttcatattat gattcagaat catttctat tgtggattta taggttggtt aaagtgtatgg 1155

cctttttagt gggtttggt gtgtcttgg aacaagtcgt tactgtgtcc attattggaa 1215

tggaatttac actactgtat catgagtgccc tattttgatt ctatggttcc ctcaagtattta 1275

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tatactcaat aaatattttt caaaagg 1362

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<211> 622

<212> PRT

<213> Homo sapiens

<400> 63

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20 25 30

Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp Asp Tyr Ser Thr

35 40 45

Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr Glu Arg Cys Arg

50 55 60

Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn

65 70 75 80

Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg Ile Asp Leu Val

85 90 95

Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln Leu Gly Gly Asp

100 105 110

Leu Asn Ser Thr Pro Leu His Trp Ala Thr Arg Gln Gly His Leu Ser

115 120 125

Met Val Val Gln Leu Met Lys Tyr Gly Ala Asp Pro Ser Leu Ile Asp

130 135 140

Gly Glu Gly Cys Ser Cys Ile His Leu Ala Ala Gln Phe Gly His Thr

145 150 155 160

Ser Ile Val Ala Tyr Leu Ile Ala Lys Gly Gln Asp Val Asp Met Met

165

170

175

Asp Gln Asn Gly Met Thr Pro Leu Met Trp Ala Ala Tyr Arg Thr His

180

185

190

Ser Val Asp Pro Thr Arg Leu Leu Leu Thr Phe Asn Val Ser Val Asn

195

200

205

Leu Gly Asp Lys Tyr His Lys Asn Thr Ala Leu His Trp Ala Val Leu

210

215

220

Ala Gly Asn Thr Thr Val Ile Ser Leu Leu Leu Glu Ala Gly Ala Asn

225

230

235

240

Val Asp Ala Gln Asn Ile Lys Gly Glu Ser Ala Leu Asp Leu Ala Lys

245

250

255

Gln Arg Lys Asn Val Trp Met Ile Asn His Leu Gln Glu Ala Arg Gln

260

265

270

Ala Lys Gly Tyr Asp Asn Pro Ser Phe Leu Arg Lys Leu Lys Ala Asp

275

280

285

Lys Glu Phe Arg Gln Lys Val Met Leu Gly Thr Pro Phe Leu Val Ile

290

295

300

Trp Leu Val Gly Phe Ile Ala Asp Leu Asn Ile Asp Ser Trp Leu Ile

305

310

315

320

Lys Gly Leu Met Tyr Gly Gly Val Trp Ala Thr Val Gln Phe Leu Ser

325 330 335

Lys Ser Phe Phe Asp His Ser Met His Ser Ala Leu Pro Leu Gly Ile

340 345 350

Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp Phe Phe Trp Phe

355 360 365

Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro Phe Leu Ala Asn

370 375 380

Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro

385 390 395 400

Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Thr Ile Val Glu

405 410 415

Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys

420 425 430

Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly Val Cys Asn Arg

435 440 445

Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val Gly Asn Cys Val

450 455 460

Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu

465 470 475 480

Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu

485 490 495

His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr

500 505 510

Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met Phe Leu Asn Ser

515 520 525

Val Phe His Phe Met Trp Val Ala Val Leu Leu Met Cys Gln Met Tyr

530 535 540

Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg Met Asn Ala Arg

545 550 555 560

Arg Tyr Lys His Phe Lys Val Thr Thr Ser Ile Glu Ser Pro Phe

565 570 575

Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys

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595 600 605

Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln Leu Val

610 615 620

<210> 64

<211> 2948

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (14)..(1879)

<400> 64

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ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc caa agc cat 97
Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His
15 20 25

tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act cat att gat 145
Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp
30 35 40

gat tac agc aca tgg gac ata gtc aag gct aca caa tat gga ata tat 193
Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr
45 50 55 60

gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta cgg caa ccg 241
Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro
65 70 75

gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc aat aac aga 289
Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg

80

85

90

ata gat tta gtc aaa tac tat att tcg aaa ggt gct att gtg gat caa 337
Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln

95

100

105

ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc aca aga caa 385
Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Thr Arg Gln

110

115

120

ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt gca gat cct 433
Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly Ala Asp Pro
125 130 135 140

tca tta att gat gga gaa gga tgt agc tgt att cat ctg gct gct cag 481
Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu Ala Ala Gln
145 150 155

ttc gga cat acc tca att gtt gct tat ctc ata gca aaa gga cag gat 529
Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys Gly Gln Asp
160 165 170

gta gat atg atg gat cag aat gga atg acg cct tta atg tgg gca gca 577
Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met Trp Ala Ala
175 180 185

tat aga aca cat agt gtg gat cca act aga ttg ctt tta aca ttc aat 625
Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Thr Phe Asn
190 195 200

gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act gct ctg cat 673
Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr Ala Leu His
205 210 215 220

tgg gca gtg cta gca ggg aat acc aca gtc att agc ctt ctt ctg gaa 721
Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu Leu Glu
225 230 235

gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa tca gcg ctt 769
Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu Ser Ala Leu
240 245 250

gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac cac tta caa 817
Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn His Leu Gln
255 260 265

gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc ctt aga aag 865
Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe Leu Arg Lys
270 275 280

ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta gga act cct 913
Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu Gly Thr Pro
285 290 295 300

ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta aat att gat 961

Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu Asn Ile Asp

305

310

315

tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg gct aca gta 1009

Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp Ala Thr Val

320

325

330

cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat agt gca ttg 1057

Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His Ser Ala Leu

335

340

345

ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat gtg acg tgg 1105

Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp

350

355

360

ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc cat ctt cca 1153

Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro

365

370

375

380

ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga aaa tct tgg 1201

Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp

385

390

395

aaa tca gat cca ggg att att aaa gca aca gaa gag caa aag aaa aag 1249

Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys

400

405

410

aca ata gtt gaa ctt gca gag aca gga agt ctg gac ctc agt ata ttc 1297

Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe

415

420

425

tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa cat tgt ggt 1345
Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly

430

435

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gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc cca tgg gtg 1393
Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val
445 450 455 460

ggt aac tgt gta ggt gca ggc aac cat aga tat ttt atg ggc tac cta 1441
Gly Asn Cys Val Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu
465 470 475

ttc ttc ttg ctt ttt atg atc tgc tgg atg att tat ggt tgt ata tct 1489
Phe Phe Leu Leu Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser
480 485 490

tac tgg gga ctc cac tgt gag acc act tac acc aag gat gga ttt tgg 1537
Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp
495 500 505

aca tac att act cag att gcc acg tgt tca cct tgg atg ttt tgg atg 1585
Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met
510 515 520

ttc ctg aac agt gtt ttc cac ttc atg tgg gtg gct gta tta ctc atg 1633
Phe Leu Asn Ser Val Phe His Phe Met Trp Val Ala Val Leu Leu Met
525 530 535 540

tgt cag atg tac cag ata tca tgt tta ggt att act aca aat gaa aga 1681

Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg

545

550

555

atg aat gcc agg aga tac aag cac ttt aaa gtc aca aca acg tct att 1729

Met Asn Ala Arg Arg Tyr Lys His Phe Lys Val Thr Thr Ser Ile

560

565

570

gaa agc cca ttc aac cat gga tgt gta aga aat att ata gac ttc ttt 1777

Glu Ser Pro Phe Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe

575

580

585

gaa ttt cga tgc tgt ggc ctc ttt cgt cct gtt atc gtg gac tgg acc 1825

Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr

590

595

600

agg cag tat aca ata gaa tat gac caa ata tca gga tct ggg tac cag 1873

Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln

605

610

615

620

ctg gtg tagcgacatc ttatcctatg aagcatattt ctgagtggtg cctgaaaatt 1929

Leu Val

gtgtctgtcc gtgtctttct cacactcgaa tccacatcct ttgaacaaga gcatgctatg 1989

tgttagggcta atggtaatt ttacagtctt ttttcaaca cttttattaa caaaagtaaa 2049

catggacaga acacactgcc atttctggga agagtaaaga tgataaaaaa taattttaat 2109

ggttcttaat gtggaaattc acaacatact caactttgg gttttgttct cacagtattt 2169

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cagtttaac taaaactaaa ttatgttat ttggctaaat gttatgtatgc agtctagtagtac 2289

gagtattgca tctaattcca ggagcattgt tttaagttga ttgacttagtt attatgtaca 2349

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cagatactat ccagtgaagc ataaattttaga atttaatttg atgttcaaaa acagttccat 2709

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taatagtat acatggatat acttcctttt aaattctcag ctgcaaaata attgttagaca 2829

aaataatggc atttaactaa agatggagca tgatctgtt acatagcaca tgtgaataaaa 2889

agaaaagctg acagtatatt ctggtttcaa taaaatgacc tatcagaaag tagaatttc 2948

<210> 65

<211> 632

<212> PRT

<213> Homo sapiens

<400> 65

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Glu Tyr Asp Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu

20 25 30

Ile Lys Pro Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly

35 40 45

Arg Lys Thr His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala

50 55 60

Thr Gln Tyr Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly

65 70 75 80

Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp

85 90 95

Ala Ala Ile Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys

100 105 110

Gly Ala Ile Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu

115

120

125

His Trp Ala Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met

130

135

140

Lys Tyr Gly Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys

145

150

155

160

Ile His Leu Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu

165

170

175

Ile Ala Lys Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr

180

185

190

Pro Leu Met Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg

195

200

205

Leu Leu Leu Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His

210

215

220

Lys Asn Thr Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val

225

230

235

240

Ile Ser Leu Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile

245

250

255

Lys Gly Glu Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp

260

265

270

Met Ile Asn His Leu Gln Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn

275

280

285

Pro Ser Phe Leu Arg Lys Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys

290

295

300

Val Met Leu Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile

305

310

315

320

Ala Asp Leu Asn Ile Asp Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly

325

330

335

Gly Val Trp Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His

340

345

350

Ser Met His Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe

355

360

365

Trp Met Tyr Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe

370

375

380

Leu Phe Ile His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr

385

390

395

400

Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr

405

410

415

Glu Glu Gln Lys Lys Lys Thr Ile Val Glu Leu Ala Glu Thr Gly Ser

420

425

430

Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys Leu Ile Arg Lys Pro Val

435

440

445

Arg Ser Lys His Cys Gly Val Cys Asn Arg Cys Ile Ala Lys Phe Asp

450

455

460

His His Cys Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg

465

470

475

480

Tyr Phe Met Gly Tyr Leu Phe Leu Leu Phe Met Ile Cys Trp Met

485

490

495

Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr

500

505

510

Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser

515

520

525

Pro Trp Met Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp

530

535

540

Val Ala Val Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly

545

550

555

560

Ile Thr Thr Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys

565

570

575

Val Thr Thr Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg

580

585

590

Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro

595

600

605

Val Ile Val Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile

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620

Ser Gly Ser Gly Tyr Gln Leu Val

625

630

<210> 66

<211> 4715

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (108).. (2003)

<400> 66

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Met Gln Arg

1

gag gag gga ttt aac acc aag atg gcg gac ggc ccg gat gag tac gat 164

Glu Glu Gly Phe Asn Thr Lys Met Ala Asp Gly Pro Asp Glu Tyr Asp

5 10 15

acc gaa gcg ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc 212

Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro

20 25 30 35

caa agc cat tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act 260

Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr

40 45 50

cat att gat gat tac agc aca tgg gac ata gtc aag gct aca caa tat 308

His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr

55 60 65

gga ata tat gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta 356

Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val

70 75 80

cgg caa ccg gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc 404

Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile

85 90 95

aat aac aga ata gat tta gtc aaa tac tat att tcg aaa ggt gct att 452

Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile

100 105 110 115

gtg gat caa ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc 500

Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala

120 125 130

aca aga caa ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt 548
Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly

135 140 145

gca gat cct tca tta att gat gga gaa gga tgt agc tgt att cat ctg 596
Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu
150 155 160

gct gct cag ttc gga cat acc tca att gtt gct tat ctc ata gca aaa 644
Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys
165 170 175

gga cag gat gta gat atg atg gat cag aat gga atg acg cct tta atg 692
Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met
180 185 190 195

tgg gca gca tat aga aca cat agt gtg gat cca act aga ttg ctt tta 740
Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu
200 205 210

aca ttc aat gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act 788
Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr
215 220 225

gct ctg cat tgg gca gtg cta gca ggg aat acc aca gtc att agc ctt 836
Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu
230 235 240

ctt ctg gaa gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa 884
Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu
245 250 255

tca gcg ctt gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac 932
Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn
260 265 270 275

cac tta caa gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc 980
His Leu Gln Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe
280 285 290

ctt aga aag ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta 1028
Leu Arg Lys Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu
295 300 305

gga act cct ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta 1076
Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu
310 315 320

aat att gat tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg 1124
Asn Ile Asp Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Val Trp
325 330 335

gct aca gta cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat 1172
Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His
340 345 350 355

agt gca ttg ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat 1220
Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr
360 365 370

gtg acg tgg ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc 1268
Val Thr Trp Phe Phe Trp Phe Asn Asp Leu Asn Phe Leu Phe Ile
375 380 385

cat ctt cca ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga 1316
His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly
390 395 400

aaa tct tgg aaa tca gat cca ggg att att aaa gca aca gaa gag caa 1364
Lys Ser Trp Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln
405 410 415

aag aaa aag aca ata gtt gaa ctt gca gag aca gg~~a~~ agt ctg gac ctc 1412
Lys Lys Lys Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu
420 425 430 435

agt ata ttc tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa 1460
Ser Ile Phe Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys
440 445 450

cat tgt ggt gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc 1508
His Cys Gly Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys
455 460 465

cca tgg gtg ggt aac tgt gta ggt gca ggc aac cat aga tat ttt atg 1556

Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg Tyr Phe Met

470

475

480

ggc tac cta ttc ttc ttg ctt ttt atg atc tgc tgg atg att tat ggt 1604

Gly Tyr Leu Phe Phe Leu Leu Phe Met Ile Cys Trp Met Ile Tyr Gly

485

490

495

tgt ata tct tac tgg gga ctc cac tgt gag acc act tac acc aag gat 1652

Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr Thr Lys Asp

500

505

510

515

gga ttt tgg aca tac att act cag att gcc acg tgt tca cct tgg atg 1700

Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met

520

525

530

ttt tgg atg ttc ctg aac agt gtt ttc cac ttc atg tgg gtg gct gta 1748

Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp Val Ala Val

535

540

545

tta ctc atg tgt cag atg tac cag ata tca tgt tta ggt att act aca 1796

Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr

550

555

560

aat gaa aga atg aat gcc agg aga tac aag cac ttt aaa gtc aca aca 1844

Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys Val Thr Thr

565

570

575

acg tct att gaa agc cca ttc aac cat gga tgt gta aga aat att ata 1892

Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg Asn Ile Ile

580

585

590

595

gac ttc ttt gaa ttt cga tgc tgt ggc ctc ttt cgt cct gtt atc gtg 1940

Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val

600

605

610

gac tgg acc agg cag tat aca ata gaa tat gac caa ata tca gga tct 1988

Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser

615

620

625

ggg tac cag ctg gtg tagcgacatc ttatcctatg aagcatattg ctgagtggtg 2043

Gly Tyr Gln Leu Val

630

cctgaaaatt gtgtctgtcc gtgtcttct cacactcgaa tccacatcct ttgaacaaga 2103

gcatgctatg tgttagggcta atggtaatt ttacagtctt ttttcaaca cttttattaa 2163

caaaaagtaaaa catggacaga acacactgcc atttctggga agagtaaaga tgataaaaaa 2223

taattttaat ggttcttaat gtggaaattc acaacatact caactttgg gtttttgtct 2283

cacagtatTTTtcacaaaaa aagggttaaac ttattctatt gacagacatg gtgtactgat 2343

cagaaatgtt cagtttaac taaaactaaa ttatgttat ttggctaat gttatgtatgc 2403

agtcttagtac gagtattgca tctaattcca ggagcattgt tttaagttga ttgactagtt 2463

attatgtaca tttcagaatg tacacataaa tactgtgtatg aaaatcatgt gattggatc 2523

tactgtgatg ttgttcaa aggaggaga aaataatgtt cacaataaaa tgtgctaaca 2583

atgttttgtt tctatcagct gttgcaatgc tgatatattt ctatccagt gaaataattt 2643

gttagtaacct tactctgagg tttacggtc tgataatgaa gcacttgcat gagtatagta 2703

agtcatgtt ttttgttcaa atttaaaagc cctgctaatt gcatgacaca ccacatagaa 2763

tgtatactag cagatactat ccagtgaagc ataaattaga atttatttt atgttcaaaa 2823

acagttccat ttttaagggt taagggtgta tttcaagaa aaggcagaac aaataatgca 2883

aaattctcag taatagtgat acatggatat acttcctttt aaattctcag ctgcaaaata 2943

attgttagaca aaataatggc atttactaa agatggagca tgatctaagt acatagcaca 3003

tgigaataaa agaaaagctg acagtatatt ctggttcaa taaaatgacc tatcagaaag 3063

tagaattca tccccaaagag tatttcagtt tatccaatat tgagtaagt ctgaaacagt 3123

tttagaaaaa atttctttt ttttaatgt gatgcactga tcaatttttgcacagcatt 3183

ttcacacctt catggtgac tactagtcac tgcttccata aatattgtt acagggtgag 3243

atttggttta ttcatcttaa gtgctgtac aaactgtggt tcgagcaacc tgtggaaat 3303

ctgtgagagg gaatggggtg ggagatgtgg ggaaatggtg gtcagactga tgacagatcc 3363

tagaccaatg taaagaatgt gtatctgtat ataaataatt tatcaaatag ttttctttt 3423

gtgtctgtgt tagtgtttt aaagctgctc atttcatttt gtccaaaccaa aaagaaaagg 3483

gagataacta atgagcttct agtgatgttc aaaattgctg ttaataggca ttataccctg 3543

caagttcaact gcatgtctga tgcttggtaa aactagtctt ccctgtaaaa tgcaagattac 3603

aggtattaaa gcaatctagt ggtatacccg cccctgcct tagtaagagg agcagtgaaa 3663

tgtatatagt tcatgttcag tatttccaag taccatttt atatagtagc ttatttgacc 3723

ataagtacaca catcaaaaaaa agattaccct tagtgatgt gtttaatat tagaaaattg 3783

gcataatgtac ttatTTTg aaaaggaaag agatgggtgt ggggtggcaa tagcattgtg 3843

ccatTTTgtc atagaatgt aaaaattggtt aactttacaa atgtcagcta gtttgacta 3903

ctaattgggg gaaatttttag ataattttta aattcaaagt tatttataaa atgctagaat 3963

ttgttttaat tttttgtatt ttgagccact tcacatgaag actcagttgc attttatcg 4023

aatacattt tatcaacagt taaagactat ggtggTTTt tcagagTTTg gctaagaatg 4083

ttgttaccat cttctttgtt tgtggtacaa tattttcagt gcaaaagaga tgtcattcag 4143

ttaaaaagac aaacctctag atgtgttaatt acatggaaaa tactagcaat gtgaatgctt 4203

ttgttagtaac catcttgttag tacctgtgaa atctataact cagaaatggt cagatggtca 4263

ggagccagct atgcagcagt ataccatctg ttaattatt ttgttaggtcc tgtgtgtgga 4323

accaactata aacccagttc taaagttgtg tatgtatggt aacctttggg aatagttctt 4383

atcaacttaa ttggatactt ttagcaaata ggaacttaat tctcagcact gaacatgaat 4443

tacttccttg gagtttttt tcattcatat ttttgggtt tccaggaatt tatttgcata 4503

taatggcgt aaaacagcat cattgtactt aagctatgga tgttttatt ttatatttc 4563

tttatttata actgtgccaa gtattattt gctacttacc gtgttatict gtggaaagaa 4623

aaacctgtaa agtgttaat aaattagccc tcctacata aattaaatgt caaaaatttg 4683

taaaatatta atcagaataa atactgactc tt 4715

<210> 67

<211> 498

<212> PRT

<213> Homo sapiens

<400> 67

Met Ala Arg Leu Glu Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu

1

5

10

15

Leu Val Ser Pro Asn Ser Ser His Ser His Ala Val Val Leu Ser Trp

20

25

30

Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu

35

40

45

Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly

50

55

60

Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr

65

70

75

80

Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr

85

90

95

Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala

100

105

110

Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met

115

120

125

Val Gln Trp Gln Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg

130

135

140

Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln

145

150

155

160

Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp

165

170

175

Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly

180

185

190

Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln

195

200

205

Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn

210

215

220

Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile

225

230

235

240

Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala

245

250

255

Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val

260

265

270

His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr

275

280

285

Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro

290

295

300

Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu

305

310

315

320

Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu

325

330

335

Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu

340 345 350

Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr

355 360 365

Met His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr

370 375 380

Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser

385 390 395 400

Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser

405 410 415

Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe

420 425 430

Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu

435 440 445

Gly Gln Met Arg Pro Glu Gly Val Gly Leu Pro Ala Glu Val Thr Gln

450 455 460

Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp

465 470 475 480

Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe

485 490 495

Ser Cys

<210> 68

<211> 1902

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22)..(1515)

<400> 68

gaaggaggga atgactccag g atg gcc cgg ctg gaa gtg att gaa ctg cct 51

Met Ala Arg Leu Glu Val Ile Glu Leu Pro

1

5

10

cat tca cct cag aac ctc ctg gtc agc cct aat tct tcc cac agc cac 99

His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His

15

20

25

gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att 147

Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile

30

35

40

ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg 195

Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val

45

50

55

cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc 243
His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly

60

65

70

ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa 291
Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu
75 80 85 90

gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct 339
Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro
95 100 105

gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg 387
Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg
110 115 120

act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag 435
Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu
125 130 135

cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc 483
His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly
140 145 150

ctt ccc gga gag tac cag cag cgaa acat acc agc ccg gag gtg aac 531
Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn
155 160 165 170

tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag 579

Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln

175

180

185

gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg 627

Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val

190

195

200

acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg 675

Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val

205

210

215

cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct 723

Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro

220

225

230

ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg 771

Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu

235

240

245

250

gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc 819

Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala

255

260

265

cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag 867

Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys

270

275

280

ttt acc gcc tac itc act tcc gtt ctg tgc ttc acc acc cct ggg gac 915

Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp

285

290

295

ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca 963

Gly Pro Pro Ser Thr Pro Gin Leu Val Trp Thr Gln Glu Asp Lys Pro

300

305

310

gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc 1011

Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu

315

320

325

330

aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc 1059

Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly

335

340

345

tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg 1107

Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr

350

355

360

cac acc ctg aac agc acg atg cac gag tac aag atc caa ggc ctc tca 1155

His Thr Leu Asn Ser Thr Met His Glu Tyr Lys Ile Gln Gly Leu Ser

365

370

375

tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc 1203

Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly

380

385

390

act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac 1251

Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp

395 400 405 410

ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc 1299

Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg

415 420 425

tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc 1347

Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile

430 435 440

tcc agg tgg att gtt gag ggg cag atg aga cct gaa ggt gtt gga tta 1395

Ser Arg Trp Ile Val Glu Gly Gln Met Arg Pro Glu Gly Val Gly Leu

445 450 455

cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca 1443

Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala

460 465 470

aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc 1491

Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser

475 480 485 490

cag aaa ctt tgg gaa ttc tct tgt tagttggta gttttactgt aattttctat 1545

Gln Lys Leu Trp Glu Phe Ser Cys

495

aaagaattca tatcatctgt taatggcgac agttttgtt tcttccttg aatttttat 1605

attctttctt tctctttttt gtttcttctt ctttgagat tttgtaatct tactgggagg 1665

gctaaagcgt ctcttatcat atcgaattgg gacaatgata gaagacaatc tttgtttgt 1725

cactctaaag aaattattgt aagatttat catcaggtat gacatttaca ccattgtatgt 1785

aggctttta aaaaatatat ccagcctgta ttgggtaag atgattctt tctgatcctg 1845

atttcctagg agttggttt tttttttta aagcataaat aaatttaatt gcatcag 1902

<210> 69

<211> 498

<212> PRT

<213> Homo sapiens

<400> 69

Met Ala Arg Leu Glu Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu

1 5 10 15

Leu Val Ser Pro Asn Ser Ser His Ser His Ala Val Val Leu Ser Trp

20 25 30

Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu

35 40 45

Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly

50 55 60

Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr

65

70

75

80

Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr

85

90

95

Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala

100

105

110

Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met

115

120

125

Val Gln Trp Gln Pro Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg

130

135

140

Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln

145

150

155

160

Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp

165

170

175

Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly

180

185

190

Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln

195

200

205

Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn

210

215

220

Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile
225 230 235 240

Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala
245 250 255

Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val
260 265 270

His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr
275 280 285

Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro
290 295 300

Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu
305 310 315 320

Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu
325 330 335

Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu
340 345 350

Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr
355 360 365

Thr His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr

370

375

380

Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser

385

390

395

400

Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser

405

410

415

Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe

420

425

430

Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu

435

440

445

Gly Gln Met Arg His Gln Gly Val Gly Leu Pro Ala Glu Val Thr Gln

450

455

460

Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp

465

470

475

480

Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe

485

490

495

Ser Cys

<210> 70

<211> 1902

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22)..(1515)

<400> 70

gaaggaggga atgactccag g atg gcc cgg ctg gaa gtg att gaa ctg cct 51
Met Ala Arg Leu Glu Val Ile Glu Leu Pro
1 5 10

cat tca cct cag aac ctc ctg gtc agc cct aat tct tcc cac agc cac 99
His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His
15 20 25

gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att 147
Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile
30 35 40

ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg 195
Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val
45 50 55

cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc 243
His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly
60 65 70

ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa 291

Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu
75 80 85 90

gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct 339
Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro
95 100 105

gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg 387
Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg
110 115 120

act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag 435
Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu
125 130 135

cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc 483
His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly
140 145 150

ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac 531
Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn
155 160 165 170

tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag 579
Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln
175 180 185

gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg 627
Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val

190

195

200

acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg 675
Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val

205

210

215

cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct 723
Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro
220 225 230

ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg 771
Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu
235 240 245 250

gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc 819
Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala

255

260

265

cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag 867
Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys
270 275 280

ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac 915
Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp
285 290 295

ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca 963
Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp Lys Pro
300 305 310

gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc 1011

Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu

315

320

325

330

aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc 1059

Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Thr Gly

335

340

345

tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg 1107

Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr

350

355

360

cac acc ctg aac agc acg cac gag tac aag atc caa ggc ctc tca 1155

His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys Ile Gln Gly Leu Ser

365

370

375

tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc 1203

Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly

380

385

390

act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac 1251

Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp

395

400

405

410

ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc 1299

Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg

415

420

425

tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc 1347
Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile
430 435 440

tcc agg tgg att gtt gag ggg cag atg aga cat caa ggt gti gga tta 1395
Ser Arg Trp Ile Val Glu Gly Gln Met Arg His Gln Gly Val Gly Leu
445 450 455

cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca 1443
Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala
460 465 470

aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc 1491
Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser
475 480 485 490

cag aaa ctt tgg gaa ttc tct tgt tagttggta gttttactgt aatttttat 1545
Gln Lys Leu Trp Glu Phe Ser Cys
495

aaagaattca tatcatctgt taatggcgac agtttttgtt tcttccttg aatttttat 1605

attctttctt tctctttttt gtttcttctt ctttagtata ttgtaatct tactgggagg 1665

gctaaagcgt ctctatcat atcgaattgg gacaatgata gaagacaatc tttgttttgt 1725

cactctaag aaattattgt aagatttat catcaggtat gacattaca ccattgatgt 1785

aggctttta aaaaatatat ccagcctgta ttgggttaag atgattctt tctgatccgt 1845

atttcctagg agttggttt tttttttta aagcataaaal aaatttaattt gcatcag 1902

<210> 71

<211> 245

<212> PRT

<213> Homo sapiens

<400> 71

Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser Met His
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Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser Met Thr
20 25 30

Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile Leu Thr
35 40 45

Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His Arg Pro
50 55 60

Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg Leu Gly
65 70 75 80

Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser Pro Pro
85 90 95

Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile Ala Asp

100

105

110

Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe Ser Tyr

115

120

125

Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys Val Ala

130

135

140

Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu Ala Glu

145

150

155

160

Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn Gly Lys

165

170

175

Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile Glu Gly

180

185

190

Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly Thr Val

195

200

205

Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile Val Arg

210

215

220

Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val Leu Gly

225

230

235

240

Gln Trp Ile Gln Arg

245

<210> 72

<211> 1551

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (127)..(861)

<400> 72

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ccaaggccccg ccgatcgcgg gcaccggagc cagccccgca gcgggtccccg cctgtctgtc 120

acgctg atg ccc gtg cag ctg tct gag cac ccg gaa tgg aat gag tct 168

Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser

1

5

10

atg cac tcc ctc cgg atc agt gtg ggg ggc ctt cct gtg ctg gcg tcc 216

Met His Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser

15

20

25

30

atg acc aag gcc gcg gac ccc cgc ttc cgc ccc cgc tgg aag gtg atc 264

Met Thr Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile

35

40

45

ctg acg ttc ttt gtg ggt gct gcc atc ctc tgg ctg ctc tgc tcc cac 312

Leu Thr Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His

50

55

60

cgc ccg gcc ccc ggc agg ccc acc cac aat gca cac aac tgg agg 360
Arg Pro Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg

65

70

75

ctc ggc cag gcg ccc gcc aac tgg tac aat gac acc tac ccc ctg tct 408
Leu Gly Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser
80 85 90

ccc cca caa agg aca ccg gct ggg att cgg tat cga atc gca gtt atc 456
Pro Pro Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile
95 100 105 110

gca gac ctg gac aca gag tca agg gcc caa gag gaa aac acc tgg ttc 504
Ala Asp Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe
115 120 125

agt tac ctg aaa aag ggc tac ctg acc ctg tca gac agt ggg gac aag 552
Ser Tyr Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys
130 135 140

gtg gcc gtg gaa tgg gac aaa gac cat ggg gtc ctg gag tcc cac ctg 600
Val Ala Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu
145 150 155

gcg gag aag ggg aga ggc atg gag cta tcc gac ctg att gtt ttc aat 648
Ala Glu Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn
160 165 170

ggg aaa ctc tac tcc gtg gat gac cg_g ac_g ggg gtc gtc tac cag atc 696

Gly Lys Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile

175

180

185

190

gaa ggc agc aaa gcc gtg ccc tgg gtg att ctg tcc gac ggc gac ggc 744

Glu Gly Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly

195

200

205

acc gtg gag aaa ggc ttc aag gcc gaa tgg ctg gca gtg cg_g gag att 792

Thr Val Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile

210

215

220

gta agg aag cg_g tgg cg_g ctg gtg aag caa gtc tca cat gtc ggc gtt 840

Val Arg Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val

225

230

235

ctt ggc caa tgg ata caa aga taaaagaaaaat gttgcctttt tcttaggaact 891

Leu Gly Gln Trp Ile Gln Arg

240

245

gtcagaaaatc ctcatgcctt tcaagacttc tgtgaatgac ttgaattttt tattccctgc 951

ctagggctcg tgaacgaggc ctgtctcttc cctggggttt ctttccatgg cctttatttc 1011

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<210> 73

<211> 352

<212> PRT

<213> Homo sapiens

<400> 73

Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly

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Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys

20 25 30

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly

35 40 45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro

50 55 60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn

65 70 75 80

Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu

85 90 95

Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp

100 105 110

Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu

115 120 125

Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro

130 135 140

Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His

145 150 155 160

Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly

165 170 175

Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly

180 185 190

Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val

195

200

205

Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln

210

215

220

Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp

225

230

235

240

Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe

245

250

255

Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu

260

265

270

Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser

275

280

285

Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val

290

295

300

Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val

305

310

315

320

Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys

325

330

335

Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser

340

345

350

<210> 74

<211> 2401

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (103)..(1158)

<400> 74

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Met Glu Ser Gly

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ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg 162

Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val

5

10

15

20

gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc 210

Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser

25

30

35

caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag 258

Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys

40

45

50

agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata 306
Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile
55 60 65

gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg 354
Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val
70 75 80

gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag 402
Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys
85 90 95 100

atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc 450
Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile
105 110 115

att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag 498
Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu
120 125 130

gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg 546
Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val
135 140 145

gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag 594
Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln
150 155 160

tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa 642

Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys
165 170 175 180

ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca 690
Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr
185 190 195

ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg 738
Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro
200 205 210

ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc 786
Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser
215 220 225

ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg 834
Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala
230 235 240

ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg 882
Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Phe Phe Ile Leu Arg
245 250 255 260

aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag 930
Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln
265 270 275

gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct 978
Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro

280

285

290

gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc 1026
Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser

295

300

305

ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc 1074
Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr

310

315

320

gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga 1122
Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg
325 330 335 340

cag gcg atc acc cgg gtg ata ccc ccg tac aac aac agc taatagttt 1168
Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser

345

350

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ggccittgga ggagcagttgg tggggtagc tgtcacctcc aggtatgatt gagggaggaa 1288

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gtgtgaacag cagaaattaa acatgttgca acc

2401

<210> 75

<211> 352

<212> PRT

<213> Homo sapiens

<400> 75

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Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys

20 25 30

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly

35 40 45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro

50 55 60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn

65 70 75 80

Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu

85 90 95

Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp

100 105 110

Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu

115

120

125

Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro

130

135

140

Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His

145

150

155

160

Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly

165

170

175

Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly

180

185

190

Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val

195

200

205

Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln

210

215

220

Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp

225

230

235

240

Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe

245

250

255

Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu

260

265

270

Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser

275

280

285

Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val

290

295

300

Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val

305

310

315

320

Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys

325

330

335

Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser

340

345

350

<210> 76

<211> 2401

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103)..(1158)

<400> 76

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Met Glu Ser Gly

I

ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg 162
Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val
5 10 15 20

gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc 210
Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser
25 30 35

caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag 258
Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys
40 45 50

agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata 306
Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile
55 60 65

gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg 354
Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val
70 75 80

gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag 402
Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys
85 90 95 100

atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc 450
Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile
105 110 115

att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag 498
Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu
120 125 130

gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg 546
Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val
135 140 145

gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag 594
Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln
150 155 160

tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa 642
Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys
165 170 175 180

ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca 690
Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr
185 190 195

ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg 738
Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro
200 205 210

ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc 786

Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser

215

220

225

ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg 834

Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala

230

235

240

ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cg 882

Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg

245

250

255

260

aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag 930

Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln

265

270

275

gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct 978

Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro

280

285

290

gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc 1026

Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser

295

300

305

ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc 1074

Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr

310

315

320

gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga 1122

Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg

325

330

335

340

cag gcg atc acc cgg gtg ata ccc ctg tac aac agc taatagttt 1168
Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser

345

350

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ggcctttgga ggagcagtgg tggggtagc tgtcacctcc aggtatgatt gagggaggaa 1288

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gaactcctgc cacttggag agctcggtt ggtcccttgtt ttccctctt ggagaatgag 1948

gcgcagagggc ctgccttcctt gaaggacgca gtgtggatgc cactggccta gtgtcctggc 2008

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tgcctcttg gggctccctc atccagcccc tcgcagcttt gacatcttgg tgcactcatg 2128

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gagcctttta gtgcaagaca gatggggctg ttttccccca cctctgagta gttggaggtc 2248

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<212> PRT

<213> Homo sapiens

<400> 77

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Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met His Ser Ser

20 25 30

Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu Val Ala Ile

35 40 45

Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn Ser Leu Ile

50 55 60

Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile Ala Ser Ile

65 70 75 80

Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser Leu Ser Asn

85 90 95

Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp Asn Ser

100 105 110

Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu

115 120 125

Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg Ile Ser

130 135 140

Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu Phe Leu

145 150 155 160

Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val Glu Lys

165 170 175

Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu Ile Ile

180

185

190

Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val Ile Phe

195

200

205

Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile

210

215

220

Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp

225

230

235

240

Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro Phe Leu

245

250

255

Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala Gly Met

260

265

270

Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr

275

280

285

His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe

290

295

300

Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly Phe His

305

310

315

320

Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg Thr Asp

325

330

335

Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg His Phe

340

345

350

Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala Thr Ala

355

360

365

Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser

370

375

380

Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly Leu Phe

385

390

395

400

His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile

405

410

415

Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu

420

425

430

Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly Met Leu

435

440

445

Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr Tyr Gly

450

455

460

Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His Ser Lys

465

470

475

480

Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg His Asp

485 490

495

Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly Glu Trp

500 505

510

Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp

515 520 525

Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile Val Leu

530 535 540

Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys Ile Asn

545 550 555 560

Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr Val Asp

565 570 575

Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp

580 585 590

Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys

595 600 605

Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp Ser Asp

610 615 620

Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His Trp Met

625 630 635 640

Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala Asn Trp
645 650 655

Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys
660 665 670

Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu Asp Thr
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Gly Gln Gly Phe Lys Leu Val Lys Ser
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ggcgtgccgc ctccctgttc tcagtcgcag gctgaaggct tgtctgctct cctcctttt 180

ggtttggttt tggaactgac tccgagggtt gggagagcgc gttgggtggcg acggccgagt 240

cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgccgataca 300

ttggatatac tggatgaaat acaagcggtt aattttgta acgtgaggga aaagcccaca 360

ttgctggta c atg tgt aaa tca ctg cgt tat tgc ttt agt cat tgt ctc 410

Met Cys Lys Ser Leu Arg Tyr Cys Phe Ser His Cys Leu

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tat tta gca atg aca aga ctg gaa gaa gta aat aga gaa gtg aac atg 458

Tyr Leu Ala Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met

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25

cat tct tca gtg cggttat ctt ggc tat tta gcc aga atc aat tta ttg 506

His Ser Ser Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu

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35

40

45

gtt gct ata tgc tta ggt cta tac gta aga tgg gaa aaa aca gca aat 554

Val Ala Ile Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn

50

55

60

tcc tta att ttg gta att ttt att ctt ggt ctt ttt gtt ctt gga atc 602

Ser Leu Ile Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile

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70

75

gcc agc ata ctc tat tac tat ttt tca atg gaa gca gca agt tta agt 650

Ala Ser Ile Leu Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser

80	85	90	
ctc tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt 698			
Leu Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu			
95	100	105	
gat aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat 746			
Asp Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr			
110	115	120	125
ttg ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag 794			
Leu Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu			
130	135	140	
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Arg Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val			
145	150	155	
gaa ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg 890			
Glu Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu			
160	165	170	
gtg gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg 938			
Val Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met			
175	180	185	
ctg att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta 986			
Leu Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu			
190	195	200	205

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Val Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys

210 215 220

aat ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct 1082
Asn Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro
225 230 235

ttc ctt gac att tat ttt agt gga ctt tca gta act gaa aga agg aaa 1130
Phe Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys
240 245 250

ccc ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt 1178
Pro Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe
255 260 265

gct gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt 1226
Ala Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu
270 275 280 285

aga gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt 1274
Arg Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe
290 295 300

gga att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg 1322
Gly Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp
305 310 315

gga ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac 1370
Gly Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His

320 325 330

agg aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg 1418
Arg Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met
335 340 345

cgc cat ttt tgc ttg att tca gag cag ttg gtg ttc ttt agt ctt ctt 1466
Arg His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu
350 355 360 365

gca aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att 1514
Ala Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile
370 375 380

ttc ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat 1562
Phe Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His
385 390 395

ggg ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga 1610
Gly Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly
400 405 410

tat gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca 1658
Tyr Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro
415 420 425

aca ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act 1706

Thr Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr
430 435 440 445

ggc atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag 1754
Gly Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu
450 455 460

acc tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg 1802
Thr Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu
465 470 475

cat tcc aaa cta aaa gct ttc ctc gaa ctt cg^g aca gtg gat gga ccc 1850
His Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro
480 485 490

aga cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca 1898
Arg His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr
495 500 505

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Gly Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu
510 515 520 525

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Ile Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile
530 535 540

atc gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg 2042
Ile Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg

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550

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aaa attaat gac cag tat att gca gtg caa gga gca gag ttg ata aaa 2090
Lys Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys

560

565

570

aca gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca 2138
Thr Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr

575

580

585

aaa gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg 2186
Lys Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp
590 595 600 605

act gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg 2234
Thr Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg

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615

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Trp Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys
625 630 635

cac tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg 2330
His Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu
640 645 650

gca aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt 2378
Ala Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys
655 660 665

ttt agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg 2426

Phe Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val

670 675 680 685

ctg gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttggac 2472

Leu Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser

690 695

cccaaagcgg gatattaata agcactcata ctaccaatta tcactaactt gccatffff 2532

gtatgctgta tttttatgg tggaaaatac cttgctactt ctgttagctgc tctactttg 2592

tctttctta agtaattatg gtatatataa ggcgttggaa aaaaacattt tataatgaaa 2652

gtatgttaggg agtcaaatgc ttactgtaaa tgcataagag acgttaaaaa taacactgca 2712

ctttcagggaa tggttgctta tggcctgtat tagaaagaaa cagttgtcta tgctctgcaa 2772

tggtaatga tgaattacta atgccttatt ttctaggcat ataataatag ttttagagaat 2832

gtagaccaga taaatttgtt tactgtttt aaaaaactac cagtttactt acagaagatt 2892

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<212> PRT

<213> Homo sapiens

<400> 79

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Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu Thr Ser Ile Val Leu Arg

35 40 45

Ile Leu Cys Ser Leu Val Glu Arg Ile Ser Gly Tyr Val Arg His Arg

50 55 60

Pro Thr Leu Leu Thr Thr Val Glu Phe Leu Glu Leu Val Gly Phe Ala

65 70 75 80

Ile Ala Ser Thr Thr Met Leu Val Glu Lys Ser Leu Ser Val Ile Leu

85 90 95

Leu Val Val Ala Leu Ala Met Leu Ile Ile Asp Leu Arg Met Lys Ser

100 105 110

Phe Leu Ala Ile Pro Asn Leu Val Ile Phe Ala Val Leu Leu Phe Phe

115 120 125

Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile Ala Phe Ala Cys Phe Phe

130 135 140

Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp Ile Tyr Phe Ser Gly Leu

145 150 155 160

Ser Val Thr Glu Arg Trp Lys Pro Phe Leu Tyr Arg Gly Arg Ile Cys

165 170 175

Arg Arg Leu Ser Val Val Phe Ala Gly Met Ile Glu Leu Thr Phe Phe

180 185 190

Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr His Leu Trp Tyr Phe Val

195 200 205

Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe Trp Met Ile Cys His Ile

210 215 220

Ile Phe Leu Leu Thr Leu Trp Gly Phe His Thr Lys Leu Asn Asp Cys

225 230 235 240

His Lys Val Tyr Phe Thr His Arg Thr Asp Tyr Asn Ser Leu Asp Arg

245 250 255

Ile Met Ala Ser Lys Gly Met Arg His Phe Cys Leu Ile Ser Glu Gln

260 265 270

Leu Val Phe Phe Ser Leu Leu Ala Thr Ala Ile Leu Gly Ala Val Ser

275 280 285

Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser Met Phe Leu Ile Val Leu

290 295 300

Pro Leu Glu Ser Met Ala His Gly Leu Phe His Glu Leu Gly Asn Cys

305 310 315 320

Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile Val Ile Pro Thr Asn Phe

325 330 335

Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu Pro Pro Glu His Val Gln

340 345 350

Glu Leu Asn Leu Arg Ser Thr Gly Met Leu Asn Ala Ile Gln Arg Phe

355 360 365

Phe Ala Tyr His Met Ile Glu Thr Tyr Gly Cys Asp Tyr Ser Thr Ser

370 375 380

Gly Leu Ser Phe Asp Thr Leu His Ser Lys Leu Lys Ala Phe Leu Glu

385 390 395 400

Leu Arg Thr Val Asp Gly Pro Arg His Asp Thr Tyr Ile Leu Tyr Tyr

405 410 415

Ser Gly His Thr His Gly Thr Gly Glu Trp Ala Leu Ala Gly Gly Asp

420 425 430

Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp Trp Arg Glu Lys Asn Gly

435

440

445

Ser Phe Cys Ser Arg Leu Ile Ile Val Leu Asp Ser Glu Asn Ser Thr

450

455

460

Pro Trp Val Lys Glu Val Arg Lys Ile Asn Asp Gln Tyr Ile Ala Val

465

470

475

480

Gln Gly Ala Glu Leu Ile Lys Thr Val Asp Ile Glu Glu Ala Asp Pro

485

490

495

Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp Val Glu Tyr Asn Cys Asn

500

505

510

Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys Gly Arg Thr Val Lys Ala

515

520

525

Val Tyr Gly Val Ser Lys Arg Trp Ser Asp Tyr Thr Leu His Leu Pro

530

535

540

Thr Gly Ser Asp Val Ala Lys His Trp Met Leu His Phe Pro Arg Ile

545

550

555

560

Thr Tyr Pro Leu Val His Leu Ala Asn Trp Leu Cys Gly Leu Asn Leu

565

570

575

Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys Leu Lys Arg Leu Lys Met

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585

590

Ser Trp Phe Leu Pro Thr Val Leu Asp Thr Gly Gln Gly Phe Lys Leu

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Val Lys Ser

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<210> 80

<211> 3007

<212> DNA

<213> Homo sapiens

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<222> (629).. (2461)

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ggcgtgcccgc ctccctgttc tcagtcgcag gctgaaggct tgtctgctct cctccctttt 180

ggtttggttt tggaactgac tccgagggtt gggagagcgc gtgggtggcg acggccgagt 240

cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgcggataca 300

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ttgctggta catgtataa tcactgcgtt attgcttag tcattgtctc tatttagcaa 420

tgacaagact ggaagaagta aatagagaag tgaacatgca ttcttcagtg cggtatctg 480

ctattagcc agaatcaatt tattggttgc tataatgcata ggtctatacg taagatggaa 540

aaaaacagca aattccttaa ttttggtaat ttttattctt ggtcttttg ttcttgaaat 600

cgccagcata ctcttattact attttca atg gaa gca gca agt tta agt ctc 652

Met Glu Ala Ala Ser Leu Ser Leu

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tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt gat 700

Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp

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aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat ttg 748

Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu

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35

40

ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag aga 796

Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg

45

50

55

att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt gaa 844

Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu

60

65

70

ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg gtg 892

Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val

75

80

85

gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg ctg 940

Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu

90

95

100

att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta gtt 988

Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val

105

110

115

120

att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa aat 1036

Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn

125

130

135

ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct ttc 1084

Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe

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145

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ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa ccc 1132

Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro

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160

165

ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt gct 1180

Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala

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175

180

gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt aga 1228

Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg

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190

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gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt gga 1276
Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly

205

210

215

att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg gga 1324
Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly

220

225

230

ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac agg 1372
Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg

235

240

245

aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg cgc 1420
Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg

250

255

260

cat ttt tgc ttg att tca gag cag ttg gtg ttc ttt agt ctt ctt gca 1468
His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala

265

270

275

280

aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att ttc 1516
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285

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295

ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat ggg 1564
Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly

300

305

310

ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga tat 1612

Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr

315

320

325

gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca aca 1660

Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr

330

335

340

ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act ggc 1708

Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly

345

350

355

360

atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag acc 1756

Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr

365

370

375

tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg cat 1804

Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His

380

385

390

tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc aga 1852

Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg

395

400

405

cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca gga 1900

His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly

410

415

420

gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt ata 1948

Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile

425 430 435 440

gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att atc 1996

Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile

445 450 455

gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg aaa 2044

Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys

460 465 470

att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa aca 2092

Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr

475 480 485

gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca aaa 2140

Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys

490 495 500

gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg act 2188

Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr

505 510 515 520

gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg tgg 2236

Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp

525 530 535

agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag cac 2284

Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His

540

545

550

tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg gca 2332

Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala

555

560

565

aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt ttt 2380

Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe

570

575

580

agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg ctg 2428

Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu

585

590

595

600

gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttggac cccaaagcgg 2481

Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser

605

610

gatattaata agcactcata ctaccaatta tcactaactt gccatttttt gtatgtgtta 2541

tttttatttg tgaaaatac cttgctactt ctgttagctgc tctcaacttgc tctttctta 2601

agtaattatg gtatataaa ggcgttggaa aaaaacattt tataatgaaa gtatgttaggg 2661

agtcaaatgc ttactgtaaa tgcataagag acgtaaaaaa taacactgca ctttcaggaa 2721

tgtttgctta tggtcctgat tagaaagaaa cagtgtcta tgctctgcaa tggtcaatga 2781

tgaattacta atgccttatt ttctaggcat ataataatag tttagagaat gtagaccaga 2841

taaatttgtt tactgtttta agaaaactac cagttactt acagaagatt ctttttcca 2901

aacagtaggt ttcatccaag accatggaa gaactgcaaa ctcttctct tagaaaagaa 2961

agagggcagc ctaaaataaa cgcaaaattt gcttatactc catcac 3007

<210> 81

<211> 184

<212> PRT

<213> Homo sapiens

<400> 81

Met Thr Ser Phe Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu

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15

Gln Met Thr Val Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln

20

25

30

Ser Ile Ser Phe Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys

35

40

45

Phe Gly Arg Asn Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln

50

55

60

Val Ser Arg Val Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser

65

70

75

80

Ser Val Leu Ser Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu

85

90

95

Ile Val Asp Ser Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro

100

105

110

Tyr Arg Cys Met Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys

115

120

125

Glu Asp Gly Glu Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser

130

135

140

Pro Arg Ser Leu Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile

145

150

155

160

Pro Glu Tyr Gly Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Pro

165

170

175

Thr Glu Met Asp Glu Asn Glu Ser

180

<210> 82

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (285)..(836)

<400> 82

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gcgcgcgccc gagcgcggga ggatcggcgg ctgcggta ctggccctg gtcgggtcc 120

ccgcaccccg gggctcacac ttacccgcgc ggaggagcag cggccgggtg tccacccca 180

tcctgcgccc agtctcctcg attccctcg ctctgagccg ggagagccga acagctgaag 240

agagttcaact gactccccag ccccaggtgg gccttgtca catc atg acc agt ttt 296

Met Thr Ser Phe

1

gaa gat gct gac aca gaa gag aca gta act tgt ctc cag atg acg gtt 344

Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu Gln Met Thr Val

5

10

15

20

tac cat cct ggc cag ttg cag tgt gga ata ttt cag tca ata agt ttt 392

Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln Ser Ile Ser Phe

25

30

35

aac aga gag aaa ctc cct tcc agc gaa gtg gtg aaa ttt ggc cga aat 440

Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys Phe Gly Arg Asn

40

45

50

tcc aac atc tgt cat tat act ttt cag gac aaa cag gtt tcc cga gtt 488

Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln Val Ser Arg Val

55

60

65

cag ttt tct ctg cag ctg ttt aaa aaa ttc aac agc tca gtt ctc tcc 536

Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser Ser Val Leu Ser

70

75

80

ttt gaa ata aaa aat atg agt aaa aag acc aat ctg atc gtg gac agc 584

Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu Ile Val Asp Ser

85

90

95

100

aga gag ctg ggc tac cta aat aaa atg gac ctg cca tac agg tgc atg 632

Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro Tyr Arg Cys Met

105

110

115

gtc aga ttc gga gag tat cag ttt ctg atg gag aag gaa gat ggc gag 680

Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys Glu Asp Gly Glu

120

125

130

tca ttg gaa ttt ttt gag act caa ttt att tta tct cca aga tca ctc 728

Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser Pro Arg Ser Leu

135

140

145

ttg caa gaa aac aac tgg cca cca cac agg ccc ata ccg gag tat ggc 776

Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile Pro Glu Tyr Gly

150

155

160

act tat tcg ctc tgc tcc tcc caa agc agt tct ccg aca gaa atg gat 824

Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Pro Thr Glu Met Asp

165

170

175

180

gaa aat gag tca tgaacacaga aagtctaaga ggagaaaat gatggatgaa 876

Glu Asn Glu Ser

gagctctgtat gatgtgtat agacactaaa taagagttga ttaggtagt atattatagt 936

catctgttat gctgtgaaat ttggaattca gtattatcat tttgaagtct gtaaatttgt 996

ttagtcatta acttagtcac ctgttgtatt ctggatctac acaaaattat ttaactgct 1056

cttattaatc tgtgaggatt aatatacAAA aagtatcTT tgagatgaag tcgtttctc 1116

aaaataaggt tatattatTT tcttttctg cttgattttc atcttgttt ttgctttttt 1176

tttgtaagga accatctttt ggtttggtca catcagttca caacagccat ttgtttcaa 1236

ggtcaaggct ccaggcaggt tgtaactggt gtttgccatcc tgtcagttact tgcaacttg 1296

gaataggttc taggcttagtg tctgcgcgtc actgtggtt tagcatggga ggacttattt 1356

gagaaataact accttacttt tctatgattt cttttacag agttatagtg tgttactcc 1416

taagatgaca gttctcttttgc tctatattca gcatctaaga caaatattt aacatttaa 1476

agaaccactg tgtaagttt aggattattt acttaccaaa tttagttt gactttatg 1536

tgttatacac aatcttaaaa ttcacgaat tcacctttt aatagtatcc atgtacataa 1596

taaaatcaaa gtttaatttag c

1617

<210> 83

<211> 392

<212> PRT

<213> Homo sapiens

<400> 83

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser

1 5 10 15

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr

20 25 30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser

35 40 45

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn

50 55 60

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys

65 70 75 80

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro

85 90 95

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu

100 105 110

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val

115

120

125

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser

130

135

140

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg

145

150

155

160

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln

165

170

175

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser

180

185

190

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser

195

200

205

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met

210

215

220

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr

225

230

235

240

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser

245

250

255

Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu

260

265

270

Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr

275

280

285

Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu

290

295

300

Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly

305

310

315

320

Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala

325

330

335

Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val

340

345

350

Val Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg

355

360

365

Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro

370

375

380

Val Glu Ser Pro Val Gln Lys Val

385

390

<210> 84

<211> 1898

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119).. (1294)

<400> 84

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cgcgcgcccc ggggactcgat attccccggtt tccccctcca ccccacgcgg cctggacc 118

atg gac gcc aga tgg tgg gca gtg gtg ctg gct gcg ttc ccc tcc 166

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser

1

5

10

15

cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc 214

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr

20

25

30

cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc 262

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser

35

40

45

ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac 310

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn

50

55

60

tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt 358

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
65 70 75 80

gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc 406
Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
85 90 95

cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg 454
Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
100 105 110

ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg 502
Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
115 120 125

ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gca tca 550
Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
130 135 140

ccg ggt gag cgc ttt acg gac tcg cag ttc ctg gtg cta atg aac cga 598
Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
145 150 155 160

gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag 646
Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
165 170 175

ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc 694
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser

180

185

190

aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc 742
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser

195

200

205

ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg 790
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met

210

215

220

ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac 838
Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
225 230 235 240

ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc 886
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser

245

250

255

agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc 934
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
260 265 270

ttc aca gtg ggc tca ctg cta gaa cag ggg gcc cta ctg gag gga acc 982
Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr
275 280 285

cgc ttc atg ggg cga cac agt gag ttt gct gcc cat gcc ctg cta ctc 1030
Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu
290 295 300

tcc atc tgc tcc gca tgt ggc cag ctc ttc atc ttt tac acc att ggg 1078

Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly

305 310 315 320

cag ttt ggg gct gcc gtc ttc acc atc atc atg acc ctc cgc cag gcc 1126

Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala

325 330 335

ttt gcc atc ctt ctt tcc tgc ctt ctc tat ggc cac act gtc act gtg 1174

Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val

340 345 350

gtg gga ggg ctg ggg gtg gct gtg gtc ttt gct gcc ctc ctg ctc aga 1222

Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Arg

355 360 365

gtc tac gcg cgg ggc cgt cta aag caa cgg gga aag aag gct gtg cct 1270

Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro

370 375 380

gtt gag tct cct gtg cag aag gtt tgagggtgga aagggcctga ggggtgaagt 1324

Val Glu Ser Pro Val Gln Lys Val

385 390

gaaaataggac cctccccacca tccccttctg ctgtaacctc tgagggagct ggctgaaagg 1384

gcaaaatgca ggtgtttct cagtatcaca gaccagctc gcagcagggg attggggagc 1444

ccaggaggca gccttccctt ttgccttaag tcacccatct tccagtaagc agtttattct 1504

gagccccggg ggttagacagt cctcagttag gggtttggg gagtttgggg tcaagagagc 1564

atagtttaggt tccacagttt ctcttccac aagtccctt aagtcttgcc ctagctgtgc 1624

tctgccacct tccagactca ctcccctctg caaatacctg catttcttac cctggtgaga 1684

aaagcacaag cggtgttaggc tccaatgcgt ctttcccagg agggtaaga tggtgctgtg 1744

ctgagggaaag gggatgcaga gccctgcccc gcaccaccac ctcctatgct cctggatccc 1804

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cttataattt tattttatta aattaaattn ctgc 1898

<210> 85

<211> 432

<212> PRT

<213> Homo sapiens

<400> 85

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1

5

10

15

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr

20

25

30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser

35

40

45

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn

50

55

60

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys

65

70

75

80

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro

85

90

95

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu

100

105

110

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val

115

120

125

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser

130

135

140

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg

145

150

155

160

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln

165

170

175

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser

180

185

190

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser

195

200

205

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met

210

215

220

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr

225

230

235

240

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser

245

250

255

Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu

260

265

270

Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp

275

280

285

Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe

290

295

300

Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu

305

310

315

320

Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu

325

330

335

Phe Ala Ala His Ala Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln

340 345 350

Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr

355 360 365

Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu

370 375 380

Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val

385 390 395 400

Val Phe Ala Ala Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys

405 410 415

Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val

420 425 430

<210> 86

<211> 2018

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119).. (1414)

<400> 86

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cgcgcggccc ggggactcgc attcccggt tccccctcca ccccacgcgg cctggacc 118

atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc 166
Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser

1 5 10 15

cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc 214
Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr

20 25 30

cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc 262
Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser

35 40 45

ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac 310
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn

50 55 60

tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt 358
Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys

65 70 75 80

gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc 406
Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro

85 90 95

cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg 454
Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu

100 105 110

ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg 502
Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val

115 120 125

ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca 550
Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
130 135 140

ccg ggt gag cgc ttt acg gac tcg cag ttc ctg gtg cta atg aac cga 598
Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
145 150 155 160

gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag 646
Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
165 170 175

ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc 694
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
180 185 190

aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc 742
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
195 200 205

tcc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg 790
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
210 215 220

ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac 838
Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
225 230 235 240

ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc 886
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
245 250 255

agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc 934
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
260 265 270

atc tta ctg gca ggt tat att gct ttt gac agc ttc acc tca aac tgg 982
Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp
275 280 285

cag gat gcc ctg ttt gcc tat aag atg tca tcg gtg cag atg atg ttt 1030
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe
290 295 300

ggg gtc aat ttc ttc tcc tgc ctc ttc aca gtg ggc tca ctg cta gaa 1078
Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu
305 310 315 320

cag ggg gcc cta ctg gag gga acc cgc ttc atg ggg cga cac agt gag 1126
Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu
325 330 335

ttt gct gcc cat gcc ctg cta ctc tcc atc tgc tcc gca tgt ggc cag 1174

Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln

340

345

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ctc ttc atc ttt tac acc att ggg cag ttt ggg gct gcc gtc ttc acc 1222

Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr

355

360

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atc atc atg acc ctc cgc cag gcc ttt gcc atc ctt ctt tcc tgc ctt 1270

Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu

370

375

380

ctc tat ggc cac act gtc act gtg gtg gga ggg ctg ggg gtg gct gtg 1318

Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val

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390

395

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gtc ttt gct gcc ctc ctg ctc aga gtc tac gcg cgg ggc cgt cta aag 1366

Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys

405

410

415

caa cgg gga aag aag gct gtg cct gtt gag tct cct gtg cag aag gtt 1414

Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val

420

425

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tgagggtgga aaggccctga ggggtgaagt gaaaataggac cctcccacca tccccttctg 1474

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gaccagctct gcagcagggg attggggagc ccaggaggca gccttccctt ttgcctaag 1594

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aagttccctt aagtcttgcc cttagctgtgc tctgccacctt ccagactca ctcccctctg 1774

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ctttcccagg agggtgaaga tggtgctgtc ctgaggaaag gggatgcaga gccctgcccc 1894

gcaccaccac ctccttatgct cctggatccc taggctctgt tccatgagcc tggcaggt 1954

tttggtactt tagaaatgta actttttgtc cttataattt tattttatta aattaaatta 2014

ctgc 2018

<210> 87

<211> 235

<212> PRT

<213> Homo sapiens

<400> 87

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30

Asp Ser Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His

35

40

45

Ser Asn Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser

50

55

60

Val Glu Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys

65

70

75

80

Phe Val Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val

85

90

95

Gln Asn Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe

100

105

110

Ala Glu Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala

115

120

125

Val Asn Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu

130

135

140

Arg Asp Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser

145

150

155

160

Val Asn Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu

165

170

175

Asn Asn Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile

180

185

190

Asn Ala Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg

195

200

205

Ile Phe Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu

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Thr Arg Asn Met Val Gln Arg Gln Phe Ile Ala

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<210> 88

<211> 2717

<212> DNA

<213> Homo sapiens

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<222> (111)..(815)

<400> 88

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aatgctgag aaatacataa agtttcctc ttctgccttg gatatttata atg ggt 116

Met Gly

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atc ggg aag tct aaa ata aat tcc tgc cct ctt tct ctc tct tgg ggt 164

Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser Trp Gly

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15

aaa agg cac agt gtg gat aca agt cca gga tat cat gag tca gat tcc 212
Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser Asp Ser

20

25

30

aag aag tct gaa gat cta tcc ttg tgt aat gtt gct gag cac agc aat 260
Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His Ser Asn
35 40 45 50

aca aca gag ggg cca aca gga aag cag gag gga gct cag agc gtg gaa 308
Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser Val Glu
55 60 65

gag atg ttt gaa gaa gaa gct gaa gaa gag gtg ttc ctc aaa ttt gtg 356
Glu Met Phe Glu Glu Ala Glu Glu Val Phè Leu Lys Phe Val
70 75 80

ata ttg cat gca gaa gat gac aca gat gaa gcc ctc aga gtc cag aat 404
Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val Gln Asn
85 90 95

ctg cta caa gat gac ttt ggt atc aaa ccc gga ata atc ttt gct gag 452
Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe Ala Glu
100 105 110

atg cca tgt ggc aga cag cat tta cag aat tta gat gat gct gta aat 500
Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala Val Asn

115

120

125

130

ggg tct gca tgg aca atc tta tta ctg act gaa aac ttt tta aga gat 548
Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu Arg Asp

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140

145

act tgg tgt aat ttc cag ttc tat acg tcc cta atg aac tcc gtt aac 596
Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser Val Asn

150

155

160

agg cag cat aaa tac aac tct gtt ata ccc atg cgg ccc ctg aac aat 644
Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu Asn Asn

165

170

175

ccc ctt ccc cga gaa agg act ccc ttt gcc ctc caa acc atc aat gcc 692
Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile Asn Ala

180

185

190

tta gag gaa gaa agt cgt gga ttt cct aca caa gta gaa aga att ttt 740
Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg Ile Phe

195

200

205

210

cag gag tct gtg tat aag aca caa act ata tgg aaa gag aca aga 788
Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu Thr Arg

215

220

225

aat atg gta caa aga caa ttt att gcc tgagatgaaa cataataacat 835
Asn Met Val Gln Arg Gln Phe Ile Ala

230

235

gtggctggct cttgtttgt aaaccaaatg attaatcttc acttgagaaa gcagttcta 895

ggaaatgtt aaataaaaga gagtcac cttaaagaaa cctatggagc acaagaaaga 955

ttaatttcgt caggacagcc tataaaattt tggtactttt tcatgtttca gtaaaacttga 1015

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tgagatttag ggagcatgt ccacttgaga tcagggatgg ggtggagaat gggtcatgtc 1915

atgtaatgag aaaagccctc ttcgggatca tgagacttgg ttctagtcca atttctgccca 1975

ctgaggatga atgtaactgt gggcaaacta ttaccctcc ttatctgtg aaatgaaagg 2035

gttgaattga tggatctcta aaggcttttgc tcctctatga ggtgtgaaa aactagggac 2095

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2717

<210> 89

<211> 245

<212> PRT

<213> Homo sapiens

<400> 89

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Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly
20 25 30

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn
35 40 45

Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu
50 55 60

Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe
65 70 75 80

Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe

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90

95

Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe

100

105

110

Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys

115

120

125

Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val

130

135

140

Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg

145

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155

160

Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser

165

170

175

Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val

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185

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Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu

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Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu

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Gln Tyr Glu Ile Val

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<210> 90

<211> 1793

<212> DNA

<213> Homo sapiens

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<222> (60)..(794)

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Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys

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ttc aag agc gtt ctg cta atc tac act ttt att ttc tgg atc act ggc 155

Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly

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25

30

gtt atc ctt ctt gca gtt ggc att tgg ggc aag gtg agc ctg gag aat 203

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn

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tac ttt tct ctt tta aat gag aag gcc acc aat gtc ccc ttc gtg ctc 251

Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu

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55

60

att gct act ggt acc gtc att att ctt ttg ggc acc ttt ggt tgt ttt 299

Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe

65

70

75

80

gct acc tgc cga gct tct gca tgg atg cta aaa ctg tat gca atg ttt 347

Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe

85

90

95

ctg act ctc gtt ttt ttg gtc gaa ctg gtc gct gcc atc gta gga ttt 395

Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe

100

105

110

gtt ttc aga cat gag att aag aac agc ttt aag aat aat tat gag aag 443

Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys

115

120

125

gct ttg aag cag tat aac tct aca gga gat tat aga agc cat gca gta 491

Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val

130

135

140

gac aag atc caa aat acg ttg cat tgt tgt ggt gtc acc gat tat aga 539

Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg

145

150

155

160

gat tgg aca gat act aat tat tac tca gaa aaa gga ttt cct aag agt 587

Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser

165

170

175

tgc tgt aaa ctt gaa gat tgt act cca cag aga gat gca gac aaa gta 635

Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val

180

185

190

aac aat gaa ggt tgt ttt ata aag gtg atg acc att ata gag tca gaa 683

Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu

195

200

205

atg gga gtc gtt gca gga att tcc ttt gga gtt gct tgc ttc caa ctg 731

Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu

210

215

220

att gga atc ttt ctc gcc tac tgc ctc tct cgt gcc ata aca aat aac 779

Ile Gly Ile Phe Leu Ala Tyr Cys Leu Ser Arg Ala Ile Thr Asn Asn

225

230

235

240

cag tat gag ata gtg taacccaatg tatctgtggg cctattcctc tctaccttta 834

Gln Tyr Glu Ile Val

245

aggacattta gggccccccc tgtgaattag aaagtgcctt ggctggagaa ctgacaacac 894

tacttactga tagaccaaaa aactacacca gtaggttgat tcaatcaaga tgtatgtaga 954

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<210> 91

<211> 180

<212> PRT

<213> Homo sapiens

<400> 91

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Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu

20 25 30

Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala

35 40 45

Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg

50 55 60

Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly

65 70 75 80

Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met

85 90 95

Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys

100 105 110

Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln

115 120 125

Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu

130 135 140

Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser

145 150 155 160

Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser

165 170 175

Ala Leu Leu Gln

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<210> 92

<211> 970

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (26)..(565)

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Arg Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Gly

10 15 20 25

ata gga att ctg gtg ctc ctg atc atc gtg att ctg ggg gtg ccc ttg 148
Ile Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu

30 35 40

att atc ttc acc atc aag gcc aac agc gag gcc tgc cgg gac ggc ctt 196
Ile Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu

45 50 55

cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag 244
Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu

60 65 70

ctg acc gag gcc cag aag ggc ttt cag gat gtg gag gcc cag gct gcc 292
Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala

75 80 85

acc tgc aac cac act gtg atg gcc cta atg gct tcc ctg gat gca gag 340
Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu
90 95 100 105

aag gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act 388
Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr
110 115 120

aca tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg 436
Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu
125 130 135

aga aga gaa aac cag gtc tta agc gtg aga atc gcg gac aag aag tac 484

Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr

140

145

150

tac ccc agc tcc cag gac tcc agc tcc gct gcg gcg ccc cag ctg ctg 532

Tyr Pro Ser Ser Gln Asp Ser Ser Ala Ala Ala Pro Gln Leu Leu

155

160

165

att gtg ctg ctg ggc ctc agc gct ctg ctg cag tgagatccca ggaagctggc 585

Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln

170

175

180

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<210> 93

<211> 331

<212> PRT

<213> Homo sapiens

<400> 93

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20 25 30

Glu Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu

35 40 45

Ala Asp Ala Leu Tyr Glu Ala Leu Lys Leu Arg Thr Tyr Ala Ala

50 55 60

Ile Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp

65 70 75 80

Phe Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile

85 90 95

Glu Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly

100 105 110

Cys Thr Ile Ser Asn Val Val Ser Ser Ser Thr Gly Ala Ala Ser Gly

115 120 125

Ile Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr

130 135 140

Ser Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala

145 150 155 160

Val Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser

165 170 175

Ala Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu

180 185 190

Lys Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser

195 200 205

Leu Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile

210 215 220

Arg Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr

225 230 235 240

Trp Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala

245 250 255

Gly Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr

260 265 270

Thr Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu

275 280 285

Ser Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu

290

295

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Arg Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln

305

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315

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Ile Tyr Gln Arg Leu Asn Pro Cys His Thr His

325

330

<210> 94

<211> 2039

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (175)..(1167)

<400> 94

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tca gactg gagagctcca aggaaagtct ctca gacttggacc tggctgctgg cacc atg 177

Met

1

gac tca gaa aag aaa cgc ttt act gaa gag gcc acc aaa tac ttc cgg 225

Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe Arg

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10

15

gag aga gtc agc cca gtg cat ctg caa atc ctg ctg act aac aat gaa 273

Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn Glu

20

25

30

gcc tgg aag aga ttc gtg act gcg gct gaa ttg ccc agg gat gag gca 321

Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu Ala

35

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45

gat gct ctc tac gaa gct ctg aag aag ctt aga aca tat gca gct att 369

Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala Ile

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gag gac gaa tat gtg cag cag aaa gat gag cag ttt agg gaa tgg ttt 417

Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp Phe

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ttg aaa gag ttt ccc caa gtc aag agg aag atc cag gag tcc ata gaa 465

Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile Glu

85

90

95

aag ctt cgt gcc ctt gca aat ggt att gaa gag gtc cac aga ggc tgc 513

Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly Cys

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105

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acc atc tcc aac gtg gtg tcc agc tcc act ggc gct gcc tct ggc atc 561

Thr Ile Ser Asn Val Val Ser Ser Thr Gly Ala Ala Ser Gly Ile

115 120 125

atg tcc ctt gct ggt ctt gtt ttg gca cca ttt aca gca ggg acg agt 609

Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr Ser

130

135

140

145

ctg gcc ctt act gca gct ggg gta ggg ctg gga gca gcg tct gct gtg 657

Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala Val

150

155

160

act ggg atc acc acc agc atc gtg gag cac tca tac aca tca tca gca 705

Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ala

165

170

175

gaa gct gaa gcc agc agg ctg act gca acc agc att gac cga ttg aag 753

Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu Lys

180

185

190

gta ttt aag gaa gtt atg cgt gac atc aca ccc aac tta ctt tcc ctt 801

Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser Leu

195

200

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ctt aat aat tat tac gaa gcc aca caa acc att ggg agt gaa atc cgt 849

Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile Arg

210

215

220

225

gcc atc agg caa gcc aga gcc agg gcc cga ctc cct gtg acc acc tgg 897

Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr Trp

230

235

240

cga atc tca gct gga agt ggt ggt caa gca gag aga acg att gca ggc 945
Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala Gly

245 250 255

acc acc cgg gca gtg agc aga gga gcc cgg atc ctg agt gcg acc act 993
Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr Thr

260 265 270

tca ggc atc ttc ctt gca ctg gat gtg gtc aac ctt gta tac gag tca 1041
Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu Ser
275 280 285

aag cac ttg cat gag ggg gca aag tct gca tct gct gag gag ctg agg 1089
Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu Arg
290 295 300 305

cgg cag gct cag gag ctg gag gag aat cta atg gag ctc act cag atc 1137
Arg Gln Ala Gln Glu Leu Glu Asn Leu Met Glu Leu Thr Gln Ile
310 315 320

tat cag cgt ctg aat cca tgc cat acc cac tgacccaga ccagtgcagc 1187
Tyr Gln Arg Leu Asn Pro Cys His Thr His
325 330

cagcagggga ggtgagccat acacaggcca cgacaaaatg caggcattt attagggga 1247

taaagagggc aaggtaaagt ttatggagct gagtgttagt gacttggca tttctgttagc 1307

tgagcacagc aggggagggg ttaatgcaga tggcaagtgc accaaggaga aggccaggaat 1367

gctggagcct ggaataaggg aggagagggg actggagagt gtggggaaata ggaagaagaa 1427

atttcctta gactaacgaa tatattgggg ggaggaatag aggggaggtg tgcaggaacc 1487

agcaatgaga aggccaggaa aagaaagagc tgaaaatgca gaaagccgaa gagttagaac 1547

tttggatac agcagaagaa acagcggctc cactaccgac ctgccccgg ttcgatgtcc 1607

ttccaagaat gaagtcttgc cctgggtgatg gtccctgccc ctgtcttcc agcatccact 1667

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gaggtggtgg ttgttgtgtg atggatcccc tttaggttat ttaggggtat atgtccctg 1787

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tctctaaaaa cccaaacatc ctggagagta tgcgagaacc taccaagaaa aacagtctca 1907

ttactcaat acagcaggca aagagacaga aaattaactg aaaagcaggta tagagactgg 1967

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cacctaactca cc

2039

<210> 95

<211> 407

<212> PRT

<213> Homo sapiens

<400> 95

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Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys
20 25 30

Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg
35 40 45

Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr
50 55 60

Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu
65 70 75 80

Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly
85 90 95

His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu
100 105 110

Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe
115 120 125

Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser

130 135 140

Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg
145 150 155 160

Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr
165 170 175

Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr
180 185 190

Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys
195 200 205

Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr
210 215 220

Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys
225 230 235 240

Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg
245 250 255

Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu
260 265 270

Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp
275 280 285

Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly

290 295 300

Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu

305 310 315 320

Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu

325 330 335

Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser

340 345 350

Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser

355 360 365

Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu

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385 390 395 400

Val Cys Lys Tyr Lys Leu Leu

405

<210> 96

<211> 1409

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (181)..(1401)

<400> 96

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tttgccctgg gaaatagtaa ccctgccaaa tacatcagct ttaggagac agaggatgtg 180

atg gag ctg ctt gaa gaa gat ctc aca tgc cct att tgt tgc aat ctg 228

Met Glu Leu Leu Glu Glu Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu

1

5

10

15

ttt gat gat cca cgg gtt ttg cct tgc tcc cac aac ttc tgc aaa aaa 276

Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys

20

25

30

tgc tta gaa ggt atc tta gaa ggg agt gtg cgg aat tcc ttg tgg aga 324

Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg

35

40

45

cca gct cca ttc aag tgt cct aca tgc cgt aag gaa act tca gct act 372

Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr

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gga att aat agc ctg cag gtt aat tac tcc ctg aag ggt att gtg gaa 420

Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu

65

70

75

80

aag tat aac aag atc aag atc tct ccc aaa atg cca gta tgc aaa gga 468
Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly

85

90

95

cac ttg ggg cag cct ctc aac att ttc tgc ctg act gat atg cag ctg 516
His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu
100 105 110

att tgt ggg atc tgt gct act cgt ggg gag cac acc aaa cat gtc ttc 564
Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe
115 120 125

tgt tct att gaa gat gcc tat gct cag gaa agg gat gcc ttt gag tcc 612
Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser
130 135 140

ctc ttc cag agc ttt gag acc tgg cgt cgg gga gat gct ctt tct cgc 660
Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg
145 150 155 160

ttg gat acc ttg gaa act agt aag agg aaa tcc cta cag tta ctg act 708
Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr
165 170 175

aaa gat tca gat aaa gtg aag gaa ttt ttt gag aag tta caa cac aca 756
Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr

180

185

190

ctg gat caa aag aag aat gaa att ctg tct gac ttt gag acc atg aaa 804
Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys

195

200

205

ctt gct gtt atg caa gca tat gac cca gag atc aac aaa ctc aac acc 852
Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr

210

215

220

atc ttg cag gag caa cgg atg gcc ttt aac att gct gag gct ttc aaa 900
Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys
225 230 235 240

gat gtg tca gaa ccc att gta ttt ctg caa cag atg cag gag ttt aga 948
Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg

245

250

255

gag aaa atc aaa gta atc aag gaa act cct tta cct ccc tct aat ttg 996
Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu

260

265

270

cct gca agc cct tta atg aag aac ttt gat acc agt cag tgg gaa gac 1044
Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp

275

280

285

ata aaa cta gtc gat gtg gat aaa ctt tct ttg cct caa gac act ggc 1092
Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly

290

295

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aca ttc att agc aag att ccc tgg agc ttt tat aag tta ttt ttg cta 1140

Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu

305 310 315 320

atc ctt ctg ctt ggc ctt gtc att gtc ttt ggt cct acc atg ttc cta 1188

Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu

325 330 335

gaa tgg tca tta ttt gat gac ctg gca act tgg aaa ggc tgt ctt tca 1236

Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser

340 345 350

aac ttc agt tcc tat ctg act aaa aca gcc gat ttc ata gaa caa tca 1284

Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser

355 360 365

gtt ttt tac tgg gaa cag gtg aca gat ggg ttt ttc att ttc aat gaa 1332

Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu

370 375 380

aga ttc aag aat ttt act ttg gtg gta ctg aac aat gtg gca gaa ttt 1380

Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe

385 390 395 400

gtg tgc aaa tat aaa cta tta taaaatcg 1409

Val Cys Lys Tyr Lys Leu Leu

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<210> 97

<211> 465

<212> PRT

<213> Homo sapiens

<400> 97

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Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly

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30

His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser

35

40

45

Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala

50

55

60

Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu

65

70

75

80

Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His

85

90

95

Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys

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Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu

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Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val

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Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser

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160

Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg

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170

175

Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu

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185

190

Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr

195

200

205

Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn

210

215

220

Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser

225

230

235

240

Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp

245

250

255

Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr

260

265

270

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg

275

280

285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu

290

295

300

Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln

305

310

315

320

Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val

325

330

335

Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp

340

345

350

Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val

355

360

365

Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr

370

375

380

Leu Arg Leu Cys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro

385

390

395

400

Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu

405

410

415

Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys

420

425

430

His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro

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Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly

450

455

460

Asp

465

<210> 98

<211> 1940

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (477)..(1871)

<400> 98

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ccttggagg aggggagccc catctccccca gaagagcagt gacccagca gagaggggcc 180

tggtgtatca ctggaggaaa tagcctgccca aggaatacac gtcttcagaa gaagtctgt 240

gtggcttcaa gagactgatc aaatttgtgag aggaaaacag cctaccggc 300

tcaataaaaa atgagataat aggggitgga aggaaaacct tcaagaccta tggaagttag 360

ttgcagccag ctcatcacat agaggtgcag gtgaggtgta ttcatcac ggtggaaaat 420

tctggctgct tcatctccat ctctagagcc aatattggag ctttcaata aaagct atg 479

Met

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gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc 527

Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser

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10

15

atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac 575

Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His

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25

30

agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa 623

Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln

35

40

45

aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca 671

Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro

50

55

60

65

ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att 719

Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile

70

75

80

gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga 767
Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu His Gly
85 90 95

gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg 815
Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp
100 105 110

cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt 863
Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val
115 120 125

gaa gac gta tgc cag ggc tac aag gaa aag ctc cag gaa gct gtg aca 911
Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val Thr
130 135 140 145

aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca 959
Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr
150 155 160

gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa 1007
Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln
165 170 175

aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa 1055
Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu
180 185 190

gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg 1103
Glu Lys Ser Tyr Leu Trp Arg Leu Glu Glu Gln Gln Thr Leu

195 200 205

agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa 1151
Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu
210 215 220 225

ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc 1199
Leu Lys Ser His Ile Leu Glu Leu Glu Lys Cys Gln Gly Ser Ala
230 235 240

cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct 1247
Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala
245 250 255

gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg 1295
Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met
260 265 270

tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt 1343
Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser
275 280 285

cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta 1391
His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu
290 295 300 305

att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag 1439

Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu

310

315

320

aat cag gac aca tct tcc agg aga ttt act gcc ttc ccc tgt gtc ttg 1487

Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu

325

330

335

ggg tgt gaa ggc ttc acc tca gga aga cgt tac ttt gaa gtg gat gtt 1535

Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val

340

345

350

ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag 1583

Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln

355

360

365

agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc 1631

Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu

370

375

380

385

agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act 1679

Arg Leu Cys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr

390

395

400

tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac 1727

Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp

405

410

415

tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac 1775

Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His

420

425

430

atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat 1823
Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr

435

440

445

ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac 1871
Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp
450 455 460 465

taaggaaaag agcagaagct ccttggttta accagcacag agaaaataat ataaatccca 1931

taagggcag

1940

<210> 99

<211> 465

<212> PRT

<213> Homo sapiens

<400> 99

Met Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys
1 5 10 15

Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly
20 25 30

His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser
35 40 45

Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala

50 55 60

Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu

65 70 75 80

Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His

85 90 95

Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys

100 105 110

Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu

115 120 125

Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val

130 135 140

Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser

145 150 155 160

Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg

165 170 175

Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu

180 185 190

Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr

195

200

205

Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn

210

215

220

Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser

225

230

235

240

Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp

245

250

255

Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr

260

265

270

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg

275

280

285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu

290

295

300

Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln

305

310

315

320

Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val

325

330

335

Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp

340

345

350

Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val

355 360 365

Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr

370 375 380

Leu Arg Leu Cys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro

385 390 395 400

Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu

405 410 415

Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys

420 425 430

His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro

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ccttggaagg aggggagccc catctccccca gaagagcagt gacccagca gagaggggcc 180

tggtgtatca ctggaggaaa tagcctgccca aggaatacac gtcttcagaa gaagttctgt 240

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tcaataaaaa atgagataat aggggttgaa aggaaaacct tcaagaccta tggaaatcg 360

ttgcagccag ctcatcacat agaggtgcag gtgagggtgttcatcac ggtggaaaat 420

tctggctgct tcatctccat ctctagagcc aatattggag ctttcaata aaagct atg 479

Met

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gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc 527

Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser

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atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac 575

Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His

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agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa 623

Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln

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aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca 671

Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro

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ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att 719

Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile

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gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga 767

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gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg 815

Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp

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cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt 863

Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val

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Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val Thr

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aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca 959
Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr

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gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa 1007
Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln

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aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa 1055
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gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg 1103
Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu

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agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa 1151
Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu

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ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc 1199
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cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct 1247
Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala

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gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg 1295
Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met

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tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt 1343
Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser

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cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta 1391
His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu
290 295 300 305

att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag 1439
Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu
310 315 320

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Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val
340 345 350

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Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln
355 360 365

agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc 1631

Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu

370

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380

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agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act 1679

Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr

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tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac 1727

Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp

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410

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tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac 1775

Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His

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atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat 1823

Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr

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ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac 1871

Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp

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1940

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Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln Ser Gln
35 40 45

Ala Gln Val Pro Pro Ala Ala Pro His His His His His Ser His
50 55 60

Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr Gly Lys
65 70 75 80

Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala Lys Cys
85 90 95

Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala Lys Ile
100 105 110

Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys Ile Asp
115 120 125

Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val Val Gln

130 135 140

Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu Leu Glu

145 150 155 160

Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg Lys Val

165 170 175

Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val Ser Gly

180 185 190

Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu Lys Leu

195 200 205

Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly Asp Phe

210 215 220

Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg Thr Ile

225 230 235 240

Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys Gln Gly

245 250 255

His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met Tyr Thr

260 265 270

Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys Glu Thr

275

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285

Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser Leu Leu

290

295

300

Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn Pro Glu

305

310

315

320

Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe Leu Gln

325

330

335

Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr Val Pro

340

345

350

Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys Ala Ala

355

360

365

Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile Asp Thr

370

375

380

His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu Arg His

385

390

395

400

Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His Arg Thr

405

410

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Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser Gly Thr

420

425

430

Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg Met Ile

435

440

445

Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Glu Cys Leu Glu

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455

460

Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val Leu Arg

465

470

475

480

Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys Glu Gln

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490

495

Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr Ser Asn

500

505

510

Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly Val Leu

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520

525

Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys Thr Val

530

535

540

His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala Thr Asp

545

550

555

560

Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr Phe Ser

565

570

575

His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val

580

585

590

Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu Lys Ser

595

600

605

Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn

610

615

620

Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn Glu Glu

625

630

635

640

Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr Phe Arg

645

650

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Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys Asn Arg

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ggcgacc atg gag ctt ttg cgg act atc acc tac cag cca gcc gcc agc 169

Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser

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10

acc aaa atg tgc gag cag gcg ctg ggc aag ggt tgc gga gca gac tcg 217

Thr Lys Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser

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25

30

aag aag aag cgg ccg ccg cag ccc ccc gag gaa tcg cag cca cct cag 265

Lys Lys Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln

35

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tcc cag gcg caa gtg ccc ccg gcg gcc cct cac cac cat cac cat 313

Ser Gln Ala Gln Val Pro Pro Ala Ala Pro His His His His His

50

55

60

tcg cac tcg ggg ccg gag atc tcg cgg att atc gtc gac ccc acg act 361

Ser His Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr

65

70

75

ggg aag cgc tac tgc cgg ggc aaa gtg ctg gga aag ggt ggc ttt gca 409

Gly Lys Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Phe Ala

80

85

90

aaa tgt tac gag atg aca gat tig aca aat aac aaa gtc tac gcc gca 457
Lys Cys Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala
95 100 105 110

aaa att att cct cac agc aga gta gct aaa cct cat caa agg gaa aag 505
Lys Ile Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys
115 120 125

att gac aaa gaa ata gag ctt cac aga att ctt cat cat aag cat gta 553
Ile Asp Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val
130 135 140

gtg cag ttt tac cac tac ttc gag gac aaa gaa aac att tac att ctc 601
Val Gln Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu
145 150 155

ttg gaa tac tgc agt aga agg tca atg gct cat att ttg aaa gca aga 649
Leu Glu Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg
160 165 170

aag gtg ttg aca gag cca gaa gtt cga tac tac ctc agg cag att gtg 697
Lys Val Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val
175 180 185 190

tct gga ctg aaa tac ctt cat gaa caa gaa atc ttg cac aga gat ctc 745
Ser Gly Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu
195 200 205

aaa cta ggg aac ttt ttt att aat gaa gcc atg gaa cta aaa gtt ggg 793

Lys Leu Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly

210 215 220

gac ttc ggt ctg gca gcc agg cta gaa ccc ttg gaa cac aga agg aga 841
Asp Phe Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg

225 230 235

acg ata tgt ggt acc cca aat tat ctc tct cct gaa gtc ctc aac aaa 889
Thr Ile Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys
240 245 250

caa gga cat ggc tgt gaa tca gac att tgg gcc ctg ggc tgt gta atg 937
Gln Gly His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met
255 260 265 270

tat aca atg tta cta ggg agg ccc cca ttt gaa act aca aat ctc aaa 985
Tyr Thr Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys
275 280 285

gaa act tat agg tgc ata agg gaa gca agg tat aca atg ccg tcc tca 1033
Glu Thr Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser
290 295 300

ttg ctg gct cct gcc aag cac tta att gct agt atg ttg tcc aaa aac 1081
Leu Leu Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn
305 310 315

cca gag gat cgt ccc agt ttg gat gac atc att cga cat gac ttt ttt 1129
Pro Glu Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe

320

325

330

ttg cag ggc ttc act ccg gac aga ctg tct tct agc tgt tgt cat aca 1177
Leu Gln Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr

335 340 345 350

gtt cca gat ttc cac tta tca agc cca gct aag aat ttc ttt aag aaa 1225
Val Pro Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys

355 360 365

gca gct gct gct ctt ttt ggt ggc aaa aaa gac aaa gca aga tat att 1273
Ala Ala Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile

370 375 380

gac aca cat aat aga gtg tct aaa gaa gat gaa gac atc tac aag ctt 1321
Asp Thr His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu

385 390 395

agg cat gat ttg aaa aag act tca ata act cag caa ccc agc aaa cac 1369
Arg His Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His

400 405 410

agg aca gat gag gag ctc cag cca cct acc acc aca gtt gcc agg tct 1417
Arg Thr Asp Glu Glu Leu Gln Pro Pro Thr Thr Val Ala Arg Ser

415 420 425 430

gga aca ccc gca gta gaa aac aag cag cag att ggg gat gct att cgg 1465
Gly Thr Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg

435 440 445

atg ata gtc aga ggg act ctt ggc agc tgt agc agc agc agt gaa tgc 1513
Met Ile Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Glu Cys
450 455 460

ctt gaa gac agt acc atg gga agt gtt gca gac aca gtg gca agg gtt 1561
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465 470 475

ctt cgg gga tgt ctg gaa aac atg ccg gaa gct gat tgc att ccc aaa 1609
Leu Arg Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys
480 485 490

gag cag ctg agc aca tca ttt cag tgg gtc acc aaa tgg gtt gat tac 1657
Glu Gln Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr
495 500 505 510

tct aac aaa tat ggc ttt ggg tac cag ctc tca gac cac acc gtc ggt 1705
Ser Asn Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly
515 520 525

gtc ctt ttc aac aat ggt gct cac atg agc ctc ctt cca gac aaa aaa 1753
Val Leu Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys
530 535 540

aca gtt cac tat tac gca gag ctt ggc caa tgc tca gtt ttc cca gca 1801
Thr Val His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala
545 550 555

aca gat gct cct gag caa ttt att agt caa gtg acg gtg ctg aaa tac 1849
Thr Asp Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr
560 565 570

ttt tct cat tac atg gag gag aac ctc atg gat ggt gga gat ctg cct 1897
Phe Ser His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro
575 580 585 590

agt gtt act gat att cga aga cct cgg ctc tac ctc ctt cag tgg cta 1945
Ser Val Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu
595 600 605

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Lys Ser Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln
610 615 620

gtg aat ttc tac cat gat cat aca aaa atc atc atc tgt agc caa aat 2041
Val Asn Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn
625 630 635

gaa gaa tac ctt ctc acc tac atc aat gag gat agg ata tct aca act 2089
Glu Glu Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr
640 645 650

ttc agg ctg aca act ctg ctg atg tct ggc tgt tca tca gaa tta aaa 2137
Phe Arg Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys
655 660 665 670

aat cga atg gaa tat gcc ctg aac atg ctc tta caa aga tgt aac 2182

Asp Arg Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn

675

680

685

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2783

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2783

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<400> 103

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Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn Ser Tyr

20

25

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Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val

35

40

45

Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln

50

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Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr

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70

75

80

Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met Cys Cys

85

90

95

Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly

100

105

110

Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile

115

120

125

Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val

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Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg

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Leu

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Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser

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tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac 159

Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn

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25

30

agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg 207

Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly

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ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tcg tat tat 255

Leu Val Thr Gly Pro Asp Gly Lys Met Asn Pro Pro Ser Tyr Tyr

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55

60

acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg 303

Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr

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70

75

gtc tac gtg cag cac ccc atc acc ttt ttg gac gcg cct atc caa atg 351

Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met

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85

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tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac 399

Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn

95

100

105

110

gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg 447

Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly

115

120

125

tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag 495

Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln

130

135

140

gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac 543

Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr

145

150

155

aag cgt ttg taggacttag ccagacgtgg agggagccgg gtgcgcagg 592

Lys Arg Leu

160

aagtcccttc cacctctcat ccagcttcac gcctggtgga gtttctgccc tggtggtctc 652

acctctccag ggggccacc ttcatgtctt cttttggggg gaatacgtcg caaaactaac 712

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ctgcttccat gggcccttct ggtggcagtc tcaaacttag aagccacagt tgccatttt 952

ttgaggctgt tctgcccaga gctcggctga accagccctt agtgcctacc attatcttat 1012

ccgtctcttc ccgtccctga tgacaaagat cttgccttac agactttaca ggcttggctt 1072

ttagattctg taactgcaga ctccatttgc acacagattc acttttaattt cttaattttt 1132

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atgcattgtca gaaaaatagg gctggatctt atcactgccc tgtctccct tggatctctg 1252

tgccagatct tcagtgcccc ttccatataca gggattttt tctcatagag taattatatg 1312

aacagttttt atgacctctt ttgggtctga aatactttcg aacagaattt ctttttta 1372

aaaaaaaaaca gagatgggtt cttactatgt tgcccaggct ggtgtcgaac tcctgggctc 1432

aagcgatcct tctgccttgg cctcccgaag tgctggatt gcaggcataa gctaccatgc 1492

tgggcctgaa cataattca agaggaggat ttataaaacc attttctgtatcaaatgtat 1552

tggtgtcatt ttcccatttt ccaatgttagt ctcactt 1589

<210> 105

<211> 161

<212> PRT

<213> Homo sapiens

<400> 105

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser Ser Ala

1

5

10

15

Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn Ser Tyr

20

25

30

Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val

35

40

45

Thr Gly Pro Asp Gly Lys Met Asn Pro Pro Ser Tyr Tyr Thr Gln

50

55

60

Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr
65 70 75 80

Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met Cys Cys
85 90 95

Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly
100 105 110

Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile
115 120 125

Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val
130 135 140

Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg
145 150 155 160

Leu

<210> 106

<211> 1589

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70)..(552)

<400> 106

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ggcggtaaa atg tcg gtt cca gga cct tac cag gcg gcc act ggg cct tcc 111

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser

1 5 10

tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac 159

Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn

15 20 25 30

agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg 207

Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly

35 40 45

ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tcg tat tat 255

Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr

50 55 60

acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg 303

Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr

65 70 75

gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct gtc caa atg 351

Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met

80 85 90

tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac 399

Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn

95

100

105

110

gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg 447

Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly

115

120

125

tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag 495

Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln

130

135

140

gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac 543

Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr

145

150

155

aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg 592

Lys Arg Leu

160

aagtcctttc cacctctcat ccagcttcac gcctggtgga ggttctgccc tggtggtctc 652

acctctccag gggccccacc ttcatgtctt cttttggggg gaatacgtcg caaaactaac 712

aaatctccaa accccagaaa ttgctgcttg gagtcgtgca taggacttgc aaagacattc 772

cccttgagtg tcagttccac gttttcctgc ctccctgaga ccctgagtcc tgccatctaa 832

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aacagttttt atgacctct tttggtctga aatactttcg aacagaattt cttttttta 1372

aaaaaaaaaca gagatgggtt ttactatgt tgccaggct ggtgtcgaac tccctggctc 1432

aagcgatcct tctgccttgg cctccgaaag tgctggatt gcaggcataa gctaccatgc 1492

tgggcctgaa cataatttca agaggaggat ttataaaacc atttctgtt atcaaatgtat 1552

tggtgtcatt ttccatttg ccaatgtat ctcactt 1589

<210> 107

<211> 249

<212> PRT

<213> Homo sapiens

<400> 107

Met Ala Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val

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Leu Asp Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val

20 25 30

Val Thr Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys

35 40 45

Phe Lys Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn

50 55 60

Ser Gly Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu

65 70 75 80

Gln Pro Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met

85 90 95

Val Gln Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val

100 105 110

Trp Lys Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys

115 120 125

Val Phe Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro

130 135 140

Ser Lys Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro

145 150 155 160

Lys Pro His Ser Val Ser Leu Asn Asp Thr Glu Thr Arg Lys Leu Met

165 170 175

Glu Glu Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu

180 185 190

Asn Arg His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His

195 200 205

Ser Asp Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val

210 215 220

Thr Ser Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile

225 230 235 240

Gly Phe Phe Leu Gly Lys Phe Ile Leu

245

<210> 108

<211> 1595

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (232).. (978)

<400> 108

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gacccagcgg gtggcccacc gaaccggta cacagggca ggcgttaggg ctgggagcc 120

gcgagcctgg ctcgtccta gagctcgccg gagccgtcgc cgccgtcgtc ccccgcccc 180

agttagcaaa ccgcgcgcgc gggcgccccc ccgcgtcgct ctgtctctcc g atg gct 237

Met Ala

1

tcc gcc tca ggg gcc atg gct aag cac gag cag atc ctg gtc ctc gat 285

Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val Leu Asp

5

10

15

ccg ccc aca gac ctc aaa ttc aaa ggc ccc ttc aca gat gta gtc act 333

Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val Val Thr

20

25

30

aca aat ctt aaa ttg cga aat cca tcg gat aga aaa gtg tgt ttc aaa 381

Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys Phe Lys

35

40

45

50

gtg aag act aca gca cct cgc cgg tac tgt gtg agg ccc aac agt gga 429

Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly

55

60

65

att att gac cca ggg tca act gtg act gtt tca gta atg cta cag ccc 477
Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu Gln Pro

70

75

80

ttt gac tat gat ccg aat gaa aag agt aaa cac aag ttt atg gta cag 525
Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val Gln

85

90

95

aca att ttt gct cca cca aac act tca gat atg gaa gct gtg tgg aaa 573
Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val Trp Lys

100

105

110

gag gca aaa cct gat gaa tta atg gat tcc aaa ttg aga tgc gta ttt 621
Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys Val Phe
115 120 125 130

gaa atg ccc aat gaa aat gat aaa ttg aat gat atg gaa cct agc aaa 669
Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro Ser Lys

135

140

145

gct gtt cca ctg aat gca tct aag caa gat gga cct atg cca aaa cca 717
Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro Lys Pro
150 155 160

cac agt gtt tca ctt aat gat acc gaa aca agg aaa cta atg gaa gag 765
His Ser Val Ser Leu Asn Asp Thr Glu Thr Arg Lys Leu Met Glu Glu
165 170 175

tgt aaa aga ctt cag gga gaa atg atg aag cta tca gaa gaa aat cg^g 813
Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu Asn Arg

180 185 190

cac ctg aga gat gaa ggt tta agg ctc aga aag gta gca cat tcg gat 861
His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His Ser Asp
195 200 205 210

aaa cct gga tca acc tca act gca tcc ttc aga gat aat gtc acc agt 909
Lys Pro Gly Ser Thr Ser Ala Ser Phe Arg Asp Asn Val Thr Ser
215 220 225

cct ctt cct tca ctt ctt gtt gta att gca gcc att ttc att gga ttc 957
Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile Gly Phe
230 235 240

ttt cta ggg aaa ttc atc ttg tagagtgaag catgcagagt gctgtttctt 1008
Phe Leu Gly Lys Phe Ile Leu
245

ttttttttt tctcttgacc agaaaaagat ttgttacct accatttcat tggttagtatg 1068

gcccacggtg accattttt tgtgtgtaca gcgtcatata ggcttgcct ttaatgatct 1128

cttacggta gaaaacacaa taaaaacaaa ctgttcggct actggacagg ttgtatatta 1188

ccagatcatc actagcagat gtcagttgca cattgagtcc ttatgaaat tcataaataa 1248

agaattgttc tttctttgtg gtttaataa gagtcaaga attgttcaga gtcttgtaaa 1308

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atttagattt ctaatcccac tcattcaggaa aatgccaaaga ggtttccctt gggaaatgg 1428

tgcctcttac agtgtaaatt tttcctccctt tacctttgct aatatcatgg cagaattttt 1488

cttatccctt gtgaggcagt ttttgactga gtttttcatc ttacaatcc tgtcccatgg 1548

tattnaacat aaaaaaaaaat aaaactgtta acagattctt gctcgat 1595

<210> 109

<211> 540

<212> PRT

<213> Homo sapiens

<400> 109

Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val

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15

Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln

20

25

30

Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser

35

40

45

Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln

50 55 60

His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser

65 70 75 80

Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu

85 90 95

Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro

100 105 110

Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu

115 120 125

Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser

130 135 140

Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp

145 150 155 160

Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn

165 170 175

Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro

180 185 190

Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu

195 200 205

Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg

210 215 220

Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala

225 230 235 240

Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His

245 250 255

Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu

260 265 270

Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln

275 280 285

Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro

290 295 300

Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser

305 310 315 320

Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu

325 330 335

Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly

340 345 350

Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys

355 360 365

Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys

370 375 380

Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala

385 390 395 400

Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg

405 410 415

Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu

420 425 430

Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg

435 440 445

Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu

450 455 460

Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp

465 470 475 480

Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val

485 490 495

Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly

500 505 510

Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly

515

520

525

Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu

530

535

540

<210> 110

<211> 1810

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (102)..(1721)

<400> 110

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gaggaccac ctctgagtgt ccagtggtca gttgcggcag g atg ggg acc aca gcc 116

Met Gly Thr Thr Ala

1

5

aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 164

Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser

10

15

20

gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 212

Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His

25

30

35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga 260
Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg

40

45

50

agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt 308
Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe
55 60 65

gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct 356
Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro
70 75 80 85

ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa 404
Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu
90 95 100

gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg 452
Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu
105 110 115

ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca 500
Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro
120 125 130

ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag 548
Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln
135 140 145

cac tgc caa cag gac cggtcccaa ggg ggc tgg ggc cac cggtctg gat 596
His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp
150 155 160 165

ggc ttc ccc cct ggg cggtccat cca gac aat ctg aac caa atc tgc 644
Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys
170 175 180

ctt cct aac cgt cag cat gtgtat ggt ccc tgg aac cta cca cag 692
Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln
185 190 195

tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg 740
Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu
200 205 210

gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc 788
Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg
215 220 225

cta gag tgt gcc aaa ctt gtgtgggag gaa gca atg agc cga ttc tgt 836
Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys
230 235 240 245

gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cggt 884
Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg
250 255 260

cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca 932

Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro

265

270

275

cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg 980

His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser

280

285

290

gg t ct t gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc 1028

Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile

295

300

305

aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg 1076

Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu

310

315

320

325

cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg 1124

Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu

330

335

340

gag agg gag ttc cag cgc tgc cgc cag ggg aac aat cac acc tgt 1172

Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys

345

350

355

aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag 1220

Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu

360

365

370

tat gct gtg aag acc cac cac ttg tgt tgc cgc cac cct ccc agc 1268

Tyr Ala Val Lys Thr His His Leu Cys Cys Arg His Pro Pro Ser

375 380 385

cct act cggt gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat 1316

Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr

390 395 400 405

gac cggt gac atc ttg acc att gac atc ggt cga gtc acc ccc aac ctc 1364

Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg Val Thr Pro Asn Leu

410 415 420

atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat 1412

Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His

425 430 435

att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca 1460

Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro

440 445 450

ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc 1508

Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile

455 460 465

aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc 1556

Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu

470 475 480 485

tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc 1604

Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile

490 495 500

aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc 1652

Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala

505

510

515

aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc 1700

Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser

520

525

530

acc tct gag ccc aag gaa gaa tgagtccatc cagagcccta gagggtcaga 1751

Thr Ser Glu Pro Lys Glu Glu

535

540

tggggggaaac cccaccctgc cccacccatc tgaacactca ttacactaaa cacctcttg 1810

<210> 111

<211> 540

<212> PRT

<213> Homo sapiens

<400> 111

Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val

1

5

10

15

Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln

20

25

30

Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser

35

40

45

Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln

50

55

60

His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser

65

70

75

80

Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu

85

90

95

Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro

100

105

110

Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu

115

120

125

Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser

130

135

140

Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp

145

150

155

160

Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn

165

170

175

Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro

180

185

190

Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu
195 200 205

Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg
210 215 220

Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala
225 230 235 240

Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His
245 250 255

Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu
260 265 270

Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln
275 280 285

Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro
290 295 300

Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser
305 310 315 320

Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu
325 330 335

Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly
340 345 350

Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys
355 360 365

Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys
370 375 380

Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala
385 390 395 400

Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg
405 410 415

Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu
420 425 430

Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg
435 440 445

Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu
450 455 460

Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp
465 470 475 480

Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val
485 490 495

Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly

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Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly

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Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu

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Met Gly Thr Thr Ala

1 5

aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 164

Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser

10 15 20

gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 212
Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His
25 30 35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga 260
Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg
40 45 50

agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt 308
Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe
55 60 65

gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct 356
Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro
70 75 80 85

ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa 404
Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu
90 95 100

gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg 452
Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu
105 110 115

ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca 500
Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro
120 125 130

ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag 548

Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln

135 140 145

cac tgc caa cag gac cggtcccaa ggg ggc tgg ggc cac cggtctg gat 596

His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp

150 155 160 165

ggc ttc ccc cct ggg cggtccat cca gac aat ctg aac caa atc tgc 644

Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys

170 175 180

ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag 692

Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln

185 190 195

tcc agc tac tcc cac ctc act cgccagggaccctcaatttctgt 740

Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu

200 205 210

gag att gga tat tcc cgccgtcccac tgc cgc agc cac aca aac cgcc 788

Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg

215 220 225

cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt 836

Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys

230 235 240 245

gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cggt 884

Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg

250

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260

cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca 932
Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro

265

270

275

cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg 980
His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser

280

285

290

ggc ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc 1028
Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile

295

300

305

aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg 1076
Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu
310 315 320 325

cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg 1124
Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu
330 335 340

gag agg gag ttc cag cgc tgc cgc cag ggg aac aat cac acc tgt 1172
Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys
345 350 355

aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag 1220
Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu
360 365 370

tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc 1268

Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser

375 380 385

cct act cggt gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat 1316

Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr

390 395 400 405

gac cgg gac atc ttg acc att gac atc agt cga gtc acc ccc aac ctc 1364

Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg Val Thr Pro Asn Leu

410 415 420

atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat 1412

Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His

425 430 435

att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca 1460

Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro

440 445 450

ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc 1508

Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile

455 460 465

aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc 1556

Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu

470 475 480 485

tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc 1604
Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile
490 495 500

aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc 1652
Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala
505 510 515

aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc 1700
Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser
520 525 530

acc tct gag ccc aag gaa gaa tgagtccatc cagagcccta gagggtcaga 1751
Thr Ser Glu Pro Lys Glu Glu
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tggggggaaac cccaccctgc cccacccatc tgaacactca ttactactaaa cacctcttg 1810

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<211> 382

<212> PRT

<213> Homo sapiens

<400> 113

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30

Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu

35

40

45

Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val

50

55

60

Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu

65

70

75

80

Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val

85

90

95

Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu

100

105

110

Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys

115

120

125

Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys

130

135

140

Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu

145

150

155

160

Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile

165

170

175

Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys

180 185 190

Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile

195 200 205

Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn

210 215 220

Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val

225 230 235 240

Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro

245 250 255

Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser

260 265 270

Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu

275 280 285

Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln

290 295 300

Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met

305 310 315 320

Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp

325 330 335

Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu

340

345

350

Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser

355

360

365

Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile

370

375

380

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<211> 3074

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (201)..(1346)

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attttacttc atcctccaag gagttcaatc acttggcgtg acttcactac ttttaagcaa 180

aagagtggtg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233

Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu

1 5 10

gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca 281
Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser

15 20 25

gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca 329
Val Leu Phe Ile Phe Arg Ile Leu Leu Gly Thr Ala Val Glu Ser
30 35 40

gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct 377
Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro
45 50 55

ggt tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg 425
Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val
60 65 70 75

cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg 473
Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu
80 85 90

tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac 521
Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn
95 100 105

aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg 569
Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val
110 115 120

gac atg cac ttg aag cag att gag ata aag aag ttc aag tac ggt att 617
Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile
125 130 135

gaa gag cat ggt aag gtg aaa atg cga ggg ggg ttg ctg cga acc tac 665
Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr
140 145 150 155

atc atc agt atc ctc ttc aag tct atc ttt gag gtg gcc ttc ttg ctg 713
Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu
160 165 170

atc cag tgg tac atc tat gga ttc agc ttg agt gct gtt tac act tgc 761
Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys
175 180 185

aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc 809
Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro
190 195 200

acg gag aaa acc atc ttc atc atc ttc atg ctg gtg gtg tcc ttg gtg 857
Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val
205 210 215

tcc ctg gcc ttg aat atc att gaa ctc ttc tat gtt ttc ttc aag ggc 905
Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly
220 225 230 235

gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt 953
Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser
240 245 250

ggt gcg ctg agc cct gcc aaa gac tgt ggg tct caa aaa tat gct tat 1001
Gly Ala Leu Ser Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr
255 260 265

tgc aat ggc tgc tcc tca cca acc gct ccc ctc tcg cct atg tct cct 1049
Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro
270 275 280

cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc 1097
Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg
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aat tac aac aag caa gca agt gag caa acc tgg gct aat tac agt gca 1145
Asn Tyr Asn Lys Gln Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala
300 305 310 315

gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat 1193
Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His
320 325 330

gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta 1241
Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu
335 340 345

gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct 1289

Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro

350

355

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Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp

365

370

375

ctg gag atc tagatacagg ctgtgaaagca tcaagattcc actcaattgt 1386

Leu Glu Ile

380

ggagaagaaa aaaggtgctg tagaaagtgc accaggtgtt aattttgate cggtggaggt 1446

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ccaggaataa atacttcctg aacatcttag gtctttcaa caagaaaaag acagaggatt 1806

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atgctattac tgaaatgaat ttccttttc tgaaatgtaa tcattgtgc ttgaatgata 2526

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agaggattca gtagtacaca tacaactaat ttatggAAC tatagttga agacatctac 2826

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<212> PRT

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<400> 115

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20

25

30

Arg Ile Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu

35

40

45

Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val

50

55

60

Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu
65 70 75 80

Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val
85 90 95

Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu
100 105 110

Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys
115 120 125

Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys
130 135 140

Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu
145 150 155 160

Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile
165 170 175

Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys
180 185 190

Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile
195 200 205

Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn

210 215 220

Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val

225 230 235 240

Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro

245 250 255

Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser

260 265 270

Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu

275 280 285

Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln

290 295 300

Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met

305 310 315 320

Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp

325 330 335

Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu

340 345 350

Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser

355 360 365

Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile

370

375

380

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (201)..(1346)

<400> 116

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attttacttc atcctccaag gagttcaatc acttggcgtg acttcaatc tttaagcaa 180

aagagtggtg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233

Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu

1

5

10

gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca 281

Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser

15

20

25

gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca 329

Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser

30 35 40

gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct 377

Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro

45 50 55

ggt tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg 425

Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val

60 65 70 75

cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg 473

Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu

80 85 90

tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac 521

Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn

95 100 105

aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg 569

Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val

110 115 120

gac atg cac ttg aag cag att gag ata aag aag ttc aag tac ggt att 617

Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile

125 130 135

gaa gag cat ggt aag gtg aaa atg cga ggg ggg ttg ctg cga acc tac 665

Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr

140	145	150	155
atc atc agt atc ctc ttc aag tct atc ttt gag gtg gcc ttc ttg ctg 713 Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu			
160	165	170	
atc cag tgg tac atc tat gga ttc agc ttg agt gct gtt tac act tgc 761 Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys			
175	180	185	
aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc 809 Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro			
190	195	200	
acg gag aaa acc atc ttc atc atc atg ctg gtg gtg tcc ttg gtg 857 Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val			
205	210	215	
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220	225	230	235
gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt 953 Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser			
240	245	250	
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255	260	265	

ttc aat ggc tgc tcc tca cca acc gct ccc ctc tcg cct atg tct cct 1049
Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro

270 275 280

cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc 1097
Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg

285 290 295

aat tac aac aag caa gca agt gag caa aac tgg gct aat tac agt gca 1145
Asn Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala
300 305 310 315

gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat 1193
Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His
320 325 330

gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta 1241
Ala Gln Pro Phe Asp Phe Pro Asp Asn Gln Asn Ser Lys Lys Leu
335 340 345

gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct 1289
Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro
350 355 360

tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac 1337
Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp
365 370 375

ctg gag atc tagatacagg ctgaaagca tcaagattcc actcaattgt 1386

Leu Glu Ile

380

ggagaagaaa aaaggtgctg tagaaagtgc accaggtgtt aatttigtc cggggaggt 1446

ggtaactcaac agccttattc atgaggctta gaaaacacaa agacattaga ataccttagt 1506

tcactgggg tgtatgggt agatgggtgg agagggaggg gataagagag gtgcattgtt 1566

gtattnaaag tagtgattc aaagaactta gattataaat aagagttcca ttatgtata 1626

catagataag ggctttctt cccgcaaac accctaaga atggttctgt gtatgtaat 1686

gagcgggtgg taattgtggc taaatatttt tgtttacca agaaactgaa ataattctgg 1746

ccaggaataa atacttcctg aacatcttag gtctttcaa caagaaaaag acagaggatt 1806

gtcctaagt ccctgctaaa acattccatt tttaaaattt gcactttgaa ggttaagctt 1866

ctaggcctga ccctccaggt gtcaatggac ttgtgctact atatttttt attcttgta 1926

tcatgttaaa attcagacaa ggccccacaga ataagatttt ccatgcattt gcaaatacgt 1986

atattctttt tccatccact tgcacaatat cattaccatc actttttcat cattccttag 2046

ctactactca cattcatta atggttctg taaacatttt taagacagtt gggatgtcac 2106

ttaacatttt ttttttggc taaagtccagg gaatcaagcc atgcttaata ttaacaatc 2166

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tataaaactca caaacacaga ttigaaaata atgcacatat ggtgtcaaa ttigaacctt 2286

tctcatggat ttttgigggtg tgggccaata tggtgttac attatataat tcctgctgtg 2346

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cctacttaat acacagtaat tcagaacitg tattctatta tgattttagc agtctttgg 2706

agtgaccagc aactttgatg tttgcactaa gattttattt ggaatgcaag agaggttcaa 2766

agaggattca gtagtacaca tacaactaat ttatttgaac tatatgttga agacatctac 2826

cagtttctcc aaatgccttt tttaaaactc atcacagaag attggtgaaa atgctgagta 2886

tgacactttt ctcttgcat gcatgtcagc tacataaaca gttttgtaca atgaaaatta 2946

ctaatttgtt tgacattcca tgtaaacta cggtcatgtt cagtttcatt gcatgtaatg 3006

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<210> 117

<211> 398

<212> PRT

<213> Homo sapiens

<400> 117

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu Cys Ile Trp Met

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Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu Glu Ala Gly Ala

20 25 30

Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln

35 40 45

Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser

50 55 60

Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser

65 70 75 80

Thr Gln Asn Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly

85 90 95

Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu Arg

100 105 110

Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn

115 120 125

Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu Phe

130 135 140

Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala

145 150 155 160

Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn

165 170 175

Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val

180 185 190

Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu

195 200 205

Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr

210 215 220

Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala

225 230 235 240

His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu

245 250 255

Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr

260

265

270

Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg

275

280

285

Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro

290

295

300

Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg

305

310

315

320

Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr

325

330

335

Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu

340

345

350

Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala

355

360

365

Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile

370

375

380

Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu

385

390

395

<210> 118

<211> 2054

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76)..(1269)

<400> 118

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Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu

1

5

10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg gga gtg agg gca gag 159

Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu

15

20

25

gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act 207

Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr

30

35

40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg 255

Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met

45

50

55

60

gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag 303

Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys

65

70

75

gaa aaa gtg agc aca cag aat ctg cta ctc ctg act gat aat gag 351

Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Thr Asp Asn Glu

80

85

90

gcc tgg aac gga ttc gtg gct gct gaa ctg ccc agg aat gag gca 399

Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala

95

100

105

gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg 447

Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met

110

115

120

aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt 495

Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe

125

130

135

140

ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga 543

Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg

145

150

155

agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc 591

Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr

160

165

170

acc atc gcc aat gtg gtg tct ggc tct ctc agc att tcc tct ggc atc 639

Thr Ile Ala Asn Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile

175

180

185

ctg acc ctc gtc ggc atg ggt ctg gca ccc ttc aca gag gga ggc agc 687
Leu Thr Leu Val Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Ser

190

195

200

ctt gta ctc ttg gaa cct ggg atg gag ttg gga atc aca gca gct ttg 735
Leu Val Leu Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu
205 210 215 220

acc ggg att acc agc agt acc ata gac tac gga aag aag tgg tgg aca 783
Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr
225 230 235

caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag 831
Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys
240 245 250

gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta 879
Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu
255 260 265

gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt 927
Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg
270 275 280

gcc ctc aga cga gcc aga gaa aat ctt cag tca gta ccg cat gcc tca 975
Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser
285 290 295 300

gcc tca cgc ccc cggtc act gag cca atc tca gct gaa agc ggt gaa 1023
Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu

305 310 315

cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga 1071
Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly

320 325 330

gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat 1119
Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp

335 340 345

gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag 1167
Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys

350 355 360

tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag 1215
Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu

365 370 375 380

aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa 1263
Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln

385 390 395

gaa ctg tgaccacagg gcagggcagc caccaggaga gataatgcctg gcaggggcca 1319
Glu Leu

ggacaaaaatg caaacttttt tttttctga gacagagtct tgctctgtcg ccaagttgca 1379

gtgagccgag atatgccac tgcactccag cctgggtgac agagcgagac tccatctcaa 1439

aaaaaaaaaaa aaaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc 1499

aatgagaagg ccaggaaaag aaagagctga aaatggagaa agcccaagag tttagaacagt 1559

tggatacagg agaagaaaaca gcggctccac tacagaccca gccccaggtt caatgtcc 1619

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cccttgtcct cctggggca tatctcagtc aggcatggc ttccatgtga tggtcgttgg 1739

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acactgaagg gcaggtggtg agccatggcc atggccccca gctgaggagc aggtgtccct 1859

gagaacccaa acttcccaga gagtagtgtga gaaccaacca atgaaaacag tcccatcgct 1919

cttacccgtt aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa 1979

gctcagatct ctagagctgt ctgtccccg cccaggattt acctgtgtaa gtcccaataa 2039

actcacctac tcatac 2054

<210> 119

<211> 398

<212> PRT

<213> Homo sapiens

<400> 119

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Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu Glu Ala Gly Ala
20 25 30

Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln
35 40 45

Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser
50 55 60

Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser
65 70 75 80

Thr Gln Asn Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly
85 90 95

Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu Arg
100 105 110

Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn
115 120 125

Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu Phe
130 135 140

Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala
145 150 155 160

Leu Ala Asp Gly Val Gin Lys Val His Lys Gly Thr Thr Ile Ala Asn
165 170 175

Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val
180 185 190 -

Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu
195 200 205

Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr
210 215 220

Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala
225 230 235 240

His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu
245 250 255

Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr
260 265 270

Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg
275 280 285

Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro

290

295

300

Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg

305

310

315

320

Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr

325

330

335

Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu

340

345

350

Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala

355

360

365

Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile

370

375

380

Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu

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<210> 120

<211> 2054

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76)..(1269)

<400> 120

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aggccctgca gcgac atg gag gga gct gct ttg ctg aga gtc tct gtc ctc 111

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu

1

5

10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg aga gtg agg gca gag 159

Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu

15

20

25

gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act 207

Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr

30

35

40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg 255

Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met

45

50

55

60

gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag 303

Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys

65

70

75

gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag 351

Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Thr Asp Asn Glu

80

85

90

gcc tgg aac gga ttc gtg gct gct gaa ctg ccc agg aat gag gca 399

Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala

95

100

105

gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg 447

Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met

110

115

120

aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt 495

Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe

125

130

135

140

ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga 543

Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg

145

150

155

agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc 591

Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr

160

165

170

acc atc gcc aat gtg gtg tct ggc tct ctc agc att tcc tct ggc atc 639

Thr Ile Ala Asn Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile

175

180

185

ctg acc ctc gtc ggc atg ggt ctg gca ccc ttc aca gag gga ggc agc 687

Leu Thr Leu Val Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser

190

195

200

ctt gta ctc ttg gaa cct ggg atg gag ttg gga atc aca gca gct ttg 735

Leu Val Leu Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu

205	210	215	220
acc ggg att acc agc agt acc ata gac tac gga aag aag tgg tgg aca 783			
Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr			
225	230	235	
caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag 831			
Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys			
240	245	250	
gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta 879			
Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu			
255	260	265	
gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt 927			
Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg			
270	275	280	
gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca 975			
Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser			
285	290	295	300
gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa 1023			
Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu			
305	310	315	
cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga 1071			
Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly			
320	325	330	

gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat 1119
Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp
335 340 345

gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag 1167
Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys
350 355 360

tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag 1215
Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu
365 370 375 380

aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa 1263
Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln
385 390 395

gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcagggccca 1319
Glu Leu

ggacaaaaatg caaacttttt tttttctga gacagagtct tgctctgtcg ccaagttgca 1379

gtgagccgag atatgccac tgcactccag cctgggtgac agagcgagac tccatctcaa 1439

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aatgagaagg ccagggaaaag aaagagctga aaatggagaa agcccaagag tttagaacagt 1559

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acactgaagg gcaggtggtg agccatggcc atggtccccca gctgaggagc aggtgtccct 1859

gagaacccaa acttccaga gagtatgtga gaaccaacca atgaaaacag tcccatcgct 1919

cttaccggta aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa 1979

gctcagatct cttagatgt ctgtccccg cccaggattt acctgtgtaa gtcccaataa 2039

actcacctac tcatac 2054

<210> 121

<211> 108

<212> PRT

<213> Homo sapiens

<400> 121

Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe

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Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu

20

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Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys

35

40

45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val

50

55

60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp

65

70

75

80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala

85

90

95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu

100

105

<210> 122

<211> 1546

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (89)..(412)

<400> 122

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Met Gly Val Gln Val Glu Thr Ile

1

5

tcc cca gga gac ggg cgc acc ttc ccc aag cgc ggc cag acc tgc gtg 160

Ser Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val

10

15

20

gtg cac tac acc ggg atg ctt gaa gat gga aag aaa ttt gat tcc tcc 208

Val His Tyr Thr Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser

25

30

35

40

cgg gac aga aac aag ccc ttt aag ttt atg cta ggc aag cag gag gtg 256

Arg Asp Arg Asn Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val

45

50

55

atc cga ggc tgg gaa gaa ggg gtt gcc cag atg agt gtg ggt cag aga 304

Ile Arg Gly Trp Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg

60

65

70

gcc aaa ctg act ata tct cca gat tat gcc tat ggt gcc act ggg cac 352

Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His

75

80

85

cca ggc atc atc cca cca cat gcc act ctc gtc ttc gat gtg gag ctt 400

Pro Gly Ile Ile Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu

90

95

100

cta aaa ctg gaa tgacaggaat ggccctcctcc ctttagctccc tgggtttggaa 452

Leu Lys Leu Glu

105

tctgccatgg agggatctgg tgcctccaga catgtgcaca tgaatccata tggagctttt 512

cctgatgttc cactccactt tgtatagaca tctgccctga ctgaatgtgt tctgtcactc 572

agctttgttt ccgacacaccc tggccctct tcccccttct cctcgatgt gtgtttacct 632

aaactatatg ccataaaacct caagttactc attttatttt gttttcattt tgggttgaag 692

attcagtttc agtcttttgg atataggttt ccaattaagt acatggtcaa gtattaaacag 752

cacaagtggt aggttaacat tagaatagga attgggtttg gggggggggt ttgcaagaat 812

attttatttt aattttttgg atgaaatttt tatctattat atattaaaca ttcttgctgc 872

tgcgctgcaa agccatagca gatttgaggc gctgttgagg actgaattac tctccaagtt 932

gagagatgtc tttgggttaa attaaaagcc ctacctaataa ctgaggtggg gatggggaga 992

gcctttgcct ccaccatccc cacccacccct ccccttaaac cctctgcctt tgaaagtaga 1052

tcatgttcac tgcaatgctg gacactacag gtatctgtcc ctggggccagc agggacccct 1112

gaagcccttct ttgtggcctt ttttttttt tcatccctgtg gttttctaa tggactttca 1172

ggaattttgt aatctcataa ctttccaagc tccaccactt cctaaatctt aagaacttta 1232

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tcatgacaaa tccttgaatg ttctcttaag aaaatgatgc tggicatcgc agcttcagca 1352

tctcctgttt tttagatgctt ggctccctct gctgatctca gtttcctggc ttttcctccc 1412

tcagcccctt ctcacccctt tgctgtcctg tgttgtgatt tggtgagaaa tcgttgctgc 1472

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Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu Gly Phe Ile Ile Ala

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25

30

Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp Val Ala Asn Ser Phe

35

40

45

Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu Lys Gln Ala Cys Ile

50 55 60

Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val Leu Leu Gly Ala Lys

65 70 75 80

Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp Val Glu Met Tyr Asn

85 90 95

Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val Ser Ala Met Phe Gly

100 105 110

Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu Lys Leu Pro Ile Ser

115 120 125

Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly Phe Ser Leu Val Ala

130 135 140

Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu Ile Lys Ile Val Met

145 150 155 160

Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile Met Ser Gly Ile Leu

165 170 175

Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys Ala Asp Pro Val Pro

180 185 190

Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala Cys Thr Val Gly Ile

195 200 205

Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro Leu Leu Gly Phe Asp

210 215 220

Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser Val Gly Cys Ala Val

225 230 235 240

Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys Pro Arg Met Lys Arg

245 250 255

Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser Glu Ser Pro Leu Met

260 265 270

Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu Glu Thr Lys Leu Ser

275 280 285

Val Gly Asp Ile Glu Asn Lys His Pro Val Ser Glu Val Gly Pro Ala

290 295 300

Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg Thr Val Ser Phe Lys

305 310 315 320

Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu Arg Leu Pro Ser Val

325 330 335

Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr Val Asn Gly Ala Val

340 345 350

Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser Gln Ala Val Ser Asn

355 360 365

Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His Thr Val His Lys Asp
370 375 380

Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu His Leu Ala Lys Val
385 390 395 400

Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro Leu Arg Arg Asn Asn
405 410 415

Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly Met Pro Leu Asp Ser
420 425 430

Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu Glu Met Glu Lys Leu
435 440 445

Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile Arg Met Asp Ser Tyr
450 455 460

Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His Ser Ala Ser Glu Ile
465 470 475 480

Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly Asp Arg Lys Gly Ser
485 490 495

Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp Lys Pro Glu Val Ser
500 505 510

Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala Cys Phe Gly Ser Phe

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520

525

Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile Gly Pro Leu Val Ala

530

535

540

Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser Ser Lys Val Ala Thr

545

550

555

560

Pro Ile Trp Leu Leu Tyr Gly Gly Val Gly Ile Cys Val Gly Leu

565

570

575

Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met Gly Lys Asp Leu Thr

580

585

590

Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu Leu Ala Ser Ala Leu

595

600

605

Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro Ile Ser Thr Thr His

610

615

620

Cys Lys Val Gly Ser Val Val Ser Val Gly Trp Leu Arg Ser Lys Lys

625

630

635

640

Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe Met Ala Trp Phe Val

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Arg Tyr Val Ile Leu Arg Met

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<213> Homo sapiens

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Met Ala Thr Leu Ile Thr Ser Thr Thr Ala Ala

1

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acc gcc gct tct ggt cct ttg gtg gac tac cta tgg atg ctc atc ctg 161

Thr Ala Ala Ser Gly Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu

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ggc ttc att att gca ttt gtc ttg gca ttc tcc gtg gga gcc aat gat 209

Gly Phe Ile Ile Ala Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp

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35

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gta gca aat tct ttt ggt aca gct gtg ggc tca ggt gta gtg acc ctg 257

Val Ala Asn Ser Phe Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu

45 50 55

aag caa gcc tgc atc cta gct agc atc ttt gaa aca gtg ggc tct gtc 305

Lys Gln Ala Cys Ile Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val

60 65 70 75

tta ctg ggg gcc aaa gtg agc gaa acc atc cgg aag ggc ttg att gac 353

Leu Leu Gly Ala Lys Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp

80 85 90

gtg gag atg tac aac tcg actcaa ggg ctg ctg atg gcc ggc tca gtc 401

Val Glu Met Tyr Asn Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val

95 100 105

agt gct atg ttt ggt tct gct gtg tgg caa ctc gtg gct tcg ttt ttg 449

Ser Ala Met Phe Gly Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu

110 115 120

aag ctc cct att tct gga acc cat tgt att gtt ggt gca act att ggt 497

Lys Leu Pro Ile Ser Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly

125 130 135

ttc tcc ctc gtg gca aag ggg cag gag ggt gtc aag tgg tct gaa ctg 545

Phe Ser Leu Val Ala Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu

140 145 150 155

ata aaa att gtg atg tct tgg ttc gtg tcc cca ctg ctt tct gga att 593

Ile Lys Ile Val Met Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile

160

165

170

atg tct gga att tta ttc ttc ctg gtt cgt gca ttc atc ctc cat aag 641
Met Ser Gly Ile Leu Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys

175

180

185

gca gat cca gtt cct aat ggt ttg cga gct ttg cca gtt ttc tat gcc 689
Ala Asp Pro Val Pro Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala

190

195

200

tgc aca gtt gga ata aac ctc ttt tcc atc atg tat act gga gca ccg 737
Cys Thr Val Gly Ile Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro

205

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ttg ctg ggc ttt gac aaa ctt cct ctg tgg ggt acc atc ctc atc tcg 785
Leu Leu Gly Phe Asp Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser
220 225 230 235

gtg gga tgt gca gtt ttc tgt gcc ctt atc gtc tgg ttc ttt gta tgt 833
Val Gly Cys Ala Val Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys

240

245

250

ccc agg atg aag aga aaa att gaa cga gaa ata aag tgt agt cct tct 881
Pro Arg Met Lys Arg Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser
255 260 265

gaa agc ccc tta atg gaa aaa aag aat agc ttg aaa gaa gac cat gaa 929
Glu Ser Pro Leu Met Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu
270 275 280

gaa aca aag ttg tct ggt gat att gaa aac aag cat cct gtt tct 977
Glu Thr Lys Leu Ser Val Gly Asp Ile Glu Asn Lys His Pro Val Ser

285 290 295

gag gta ggg cct gcc act gtg ccc ctc cag gct gtg gtg gag gag aga 1025
Glu Val Gly Pro Ala Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg
300 305 310 315

aca gtc tca ttc aaa ctt gga gat ttg gag gaa gct cca gag aga gag 1073
Thr Val Ser Phe Lys Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu
320 325 330

agg ctt ccc agc gtg gac ttg aaa gag gaa acc acc agc ata gat agc acc 1121
Arg Leu Pro Ser Val Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr
335 340 345

gtg aat ggt gca gtg cag ttg cct aat ggg aac ctt gtc cag ttc agt 1169
Val Asn Gly Ala Val Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser
350 355 360

caa gcc gtc agc aac caa ata aac tcc agt ggc cac tac cag tat cac 1217
Gln Ala Val Ser Asn Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His
365 370 375

acc gtg cat aag gat tcc ggc ctg tac aaa gag cta ctc cat aaa tta 1265
Thr Val His Lys Asp Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu
380 385 390 395

cat ctt gcc aag gtg gga gat tgc atg gga gac tcc ggt gac aaa ccc 1313
His Leu Ala Lys Val Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro
400 405 410

tta agg cgc aat aat agc tat act tcc tat acc atg gca ata tgt ggc 1361
Leu Arg Arg Asn Asn Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly
415 420 425

atg cct ctg gat tca ttc cgt gcc aaa gaa ggt gaa cag aag ggc gaa 1409
Met Pro Leu Asp Ser Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu
430 435 440

gaa atg gag aag ctg aca tgg cct aat gca gac tcc aag aag cga att 1457
Glu Met Glu Lys Leu Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile
445 450 455

cga atg gac agt tac acc agt tac tgc aat gct gtg tct gac ctt cac 1505
Arg Met Asp Ser Tyr Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His
460 465 470 475

tca gca tct gag ata gac atg agt gtc aag gca gag atg ggt cta ggt 1553
Ser Ala Ser Glu Ile Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly
480 485 490

gac aga aaa gga agt aat ggc tct cta gaa gaa tgg tat gac cag gat 1601
Asp Arg Lys Gly Ser Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp
495 500 505

aag cct gaa gtc tct ctc ctc ttc cag ttc ctg cag atc ctt aca gcc 1649

Lys Pro Glu Val Ser Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala

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tgc ttt ggg tca ttc gcc cat ggt ggc aat gac gta agc aat gcc att 1697

Cys Phe Gly Ser Phe Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile

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ggg cct ctg gtt gct tta tat ttg gtt tat gac aca gga gat gtt tct 1745

Gly Pro Leu Val Ala Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser

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tca aaa gtg gca aca cca ata tgg ctt cta ctc tat ggt ggt gtt ggt 1793

Ser Lys Val Ala Thr Pro Ile Trp Leu Leu Tyr Gly Gly Val Gly

560

565

570

atc tgt gtt ggt ctg tgg gtt tgg gga aga aga gtt atc cag acc atg 1841

Ile Cys Val Gly Leu Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met

575

580

585

ggg aag gat ctg aca ccg atc aca ccc tct agt ggc ttc agt att gaa 1889

Gly Lys Asp Leu Thr Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu

590

595

600

ctg gca tct gcc ctc act gtg gtg att gca tca aat att ggc ctt ccc 1937

Leu Ala Ser Ala Leu Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro

605

610

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atc agt aca aca cat tgt aaa gtg ggc tct gtt gtg tct gtt ggc tgg 1985

Ile Ser Thr Thr His Cys Lys Val Gly Ser Val Val Ser Val Gly Trp

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625

630

635

ctc cgg tcc aag aag gct gtt gac tgg cgt ctc ttt cgt aac att ttt 2033
Leu Arg Ser Lys Lys Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe

640

645

650

atg gcc tgg ttt gtc aca gtc cct att tct gga gtt atc agt gct gcc 2081
Met Ala Trp Phe Val Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala

655

660

665

atc atg gca atc ttc aga tat gtc atc ctc aga atg tgaagctgtt 2127
Ile Met Ala Ile Phe Arg Tyr Val Ile Leu Arg Met

670

675

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atgattacag tgttaacaga agactgacaa gagtcgtttt atttgggagc cagaggaggg 2247

aagtgttact tgtgtataa ctgcgtttgt gctaaatatg aattgtctca aaatttagctg 2307

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<212> PRT

<213> Homo sapiens

<400> 125

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Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln Ala Glu Asn Ala Glu

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Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr Arg Asp Gly Phe Lys

35

40

45

Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val Ala Leu Glu Glu Glu

50 55 60

Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala Pro Val Tyr Phe Pro

65 70 75 80

Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln Asp Leu Ala Phe Trp

85 90 95

Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr Thr Pro Ala Met Gln

100 105 110

Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg Thr Glu Pro Glu Leu

115 120 125

Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly Asp Leu Ser Gly Gly

130 135 140

Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu Asp Leu Pro Ser Ser

145 150 155 160

Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn Ile Ala Ser Ala Thr

165 170 175

Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn Ser Leu Glu Met Thr

180 185 190

Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala Lys Thr Ala Phe Leu

195 200 205

Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu Leu Leu Thr His Asp

210 215 220

Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly Leu Arg Gln Arg Ala

225 230 235 240

Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu Thr Pro Arg Gly Lys

245 250 255

Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu Leu Arg Trp Val Leu

260 265 270

Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val Gly Leu Tyr Ala Met

275 280 285

<210> 126

<211> 1550

<212> DNA

<213> Homo sapiens

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<222> (81)..(944)

<400> 126

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acgagccca g caccggccgg atg gag cgt ccg caa ccc gac agc atg ccc cag 113
Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln
1 5 10

gat ttg tca gag gcc ctg aag gag gcc acc aag gag gtg cac acc cag 161
Asp Leu Ser Glu Ala Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln
15 20 25

gca gag aat gct gag ttc atg agg aac ttt cag aag ggc cag gtg acc 209
Ala Glu Asn Ala Glu Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr
30 35 40

cga gac ggc ttc aag ctg gtg atg gcc tcc ctg tac cac atc tat gtg 257
Arg Asp Gly Phe Lys Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val
45 50 55

gcc ctg gag gag att gag cgc aac aag gag agc cca gtc ttc gcc 305
Ala Leu Glu Glu Glu Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala
60 65 70 75

cct gtc tac ttc cca gaa gag ctg cac cgc aag gct gcc ctg gag cag 353
Pro Val Tyr Phe Pro Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln
80 85 90

gac ctg gcc ttc tgg tac ggg ccc cgc tgg cag gag gtc atc ccc tac 401
Asp Leu Ala Phe Trp Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr
95 100 105

aca cca gcc atg cag cgc tat gtg aag cgg ctc cac gag gtg ggg cgc 449

Thr Pro Ala Met Gln Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg

110

115

120

aca gag ccc gag ctg ctg gtg gcc cac gcc tac acc cgc tac ctg ggt 497

Thr Glu Pro Glu Leu Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly

125

130

135

gac ctg tct ggg ggc cag gtg ctc aaa aag att gcc cag aaa gcc ctg 545

Asp Leu Ser Gly Gly Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu

140

145

150

155

gac ctg ccc agc tct ggc gag ggc ctg gcc ttc ttc acc ttc ccc aac 593

Asp Leu Pro Ser Ser Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn

160

165

170

att gcc agt gcc acc aag ttc aag cag ctc tac cgc tcc cgc atg aac 641

Ile Ala Ser Ala Thr Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn

175

180

185

tcc ctg gag atg act ccc gca gtc agg cag agg gtg ata gaa gag gcc 689

Ser Leu Glu Met Thr Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala

190

195

200

aag act gcg ttc ctg ctc aac atc cag ctc ttt gag gag ttg cag gag 737

Lys Thr Ala Phe Leu Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu

205

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215

ctg ctg acc cat gac acc aag gac cag agc ccc tca cgg gca cca ggg 785

Leu Leu Thr His Asp Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly

220

225

230

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ctt cgc cag cgg gcc agc aac aaa gtg caa gat tct gcc ccc gtg gag 833
Leu Arg Gln Arg Ala Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu

240

245

250

act ccc aga ggg aag ccc cca ctc aac acc cgc tcc cag gct ccg ctt 881
Thr Pro Arg Gly Lys Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu

255

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265

ctc cga tgg gtc ctt aca ctc agc ttt ctg gtg gcg aca gtt gct gta 929
Leu Arg Trp Val Leu Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val

270

275

280

ggg ctt tat gcc atg tgaatgcagg catgtggct cccagggcca tgaaccttgt 984
Gly Leu Tyr Ala Met

285

ccgggtggaag gccttcttgc tagagaggaa attcttgg ctggcttcct taccgtggc 1044

acatgaaggct ttcatggccct ccagccctct cactgtgtcc ctctctctgg aaaggaggaa 1104

ggagccatag gcatcttccc caacgaaaag cacatccagg caatggccta aacttcagag 1164

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tcaaatgcag tattttgtt gtgttctgtt gttttatag cagggttggg gtggttttg 1464

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tgtgaaataa taaacaacat tgtctg 1550

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<211> 135

<212> PRT

<213> Homo sapiens

<400> 127

Met Ala Cys Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu

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Cys Leu Arg Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val

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30

Leu Asn Leu Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro

35

40

45

Arg Phe Asn Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys

50

55

60

Asp Gly Gly Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe

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70

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80

Gln Pro Gly Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn

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Leu Thr Val Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg

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Ile Lys Cys Val Ala Phe Asp

130

135

<210> 128

<211> 507

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (50)..(454)

<400> 128

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Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu Cys Leu Arg
5 10 15

gtg cga ggc gag gtg gct cct gac gct aag agc ttc gtg ctg aac ctg 154
Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val Leu Asn Leu
20 25 30 35

ggc aaa gac agc aac aac ctg tgc ctg cac ttc aac cct cgc ttc aac 202
Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro Arg Phe Asn
40 45 50

gcc cac ggc gac gcc aac acc atc gtg tgc aac agc aag gac ggc ggg 250
Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys Asp Gly Gly
55 60 65

gcc tgg ggg acc gag cag cgg gag gct gtc ttt ccc ttc cag cct gga 298
Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe Gln Pro Gly
70 75 80

agt gtt gca gag gtg tgc atc acc ttc gac cag gcc aac ctg acc gtc 346
Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn Leu Thr Val
85 90 95

aag ctg cca gat gga tac gaa ttc aag ttc ccc aac cgc ctc aac ctg 394
Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg Leu Asn Leu
100 105 110 115

gag gcc atc aac tac atg gca gct gac ggt gac ttc aag atc aaa tgt 442

Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys Ile Lys Cys

120

125

130

gtg gcc ttt gac tgaaatcagc cagcccatgg ccccaataa aggtagctgc 494

Val Ala Phe Asp

135

ctctgtgtccc ctg

507

<210> 129

<211> 662

<212> PRT

<213> Homo sapiens

<400> 129

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25

30

Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp

35

40

45

Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys

50

55

60

Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser

65

70

75

80

Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr

85

90

95

Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu

100

105

110

Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys

115

120

125

His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile

130

135

140

Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu

145

150

155

160

Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro

165

170

175

Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg

180

185

190

Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr

195

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Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu

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Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu
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Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu
245 250 255

Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr
260 265 270

Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln
275 280 285

Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys
290 295 300

Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val
305 310 315 320

Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala
325 330 335

Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe
340 345 350

Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp
355 360 365

Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln
370 375 380

Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp
385 390 395 400

Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu
405 410 415

Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe
420 425 430

Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn
435 440 445

Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile
450 455 460

Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp
465 470 475 480

Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu
485 490 495

Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser
500 505 510

Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr
515 520 525

Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn

530 535 540

Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly

545 550 555 560

Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln

565 570 575

Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln

580 585 590

Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn

595 600 605

Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe

610 615 620

Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn

625 630 635 640

Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg

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Leu Arg Ile Ser Glu Lys

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Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu
1 5 10

ctt att ttt aat gca gtg cat gta aaa gat gca ggc ttt tat gtc tgt 157
Leu Ile Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys
15 20 25

cga gtt aat aac aat ttc acc ttt gaa ttc agc cag tgg tca cag ctg 205
Arg Val Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu
30 35 40

gat gtt tgc gac atc cca gag agc ttc cag aga agt gtt gat ggc gtc 253
Asp Val Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val
45 50 55 60

tct gaa tcc aag ttg caa atc tgt gtt gaa cca act tcc caa aag ctg 301
Ser Glu Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu
65 70 75

atg cca ggc agc aca ttg gtt tta cag tgt gtt gct gtt gga agc cct 349
Met Pro Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro
80 85 90

att cct cac tac cag tgg ttc aaa aat gaa tta cca tta aca cat gag 397
Ile Pro His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu
95 100 105

acc aaa aag cta tac atg gtg cct tat gtg gat ttg gaa cac caa gga 445
Thr Lys Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly
110 115 120

acc tac tgg tgt cat gta tat aat gat cga gac agt caa gat agc aag 493
Thr Tyr Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys
125 130 135 140

aag gta gaa atc atc ata gga aga aca gat gag gca gtg gag tgc act 541
Lys Val Glu Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr
145 150 155

gaa gat gaa tta aat aat ctt ggt cat cct gat aat aaa gag caa aca 589
Glu Asp Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr
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act gac cag cct ttg gcg aag gac aag gtt gcc ctt ttg ata gga aat 637
Thr Asp Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn
175 180 185

atg aat tac cgg gag cac ccc aag ctc aaa gct cct ttg gtg gat gtg 685
Met Asn Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val
190 195 200

tac gaa ttg act aac tta ctg aga cag ctg gac ttc aaa gtg gtt tca 733
Tyr Glu Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser
205 210 215 220

ctg ttg gat ctt act gaa tat gag atg cgt aat gct gtg gat gag ttt 781
Leu Leu Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe
225 230 235

tta ctc ctt tta gac aag gga gta tat ggg tta tta tat tat gca gga 829
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240 245 250

cat ggt tat gaa aat ttt ggg aac agc ttc atg gtc ccc gtt gat gct 877
His Gly Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala
255 260 265

cca aat cca tat agg tct gaa aat tgt ctg tgt gta caa aat ata ctg 925
Pro Asn Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu
270 275 280

aaa ttg atg caa gaa aaa gaa act gga ctt aat gtg ttc tta ttg gat 973
Lys Leu Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp
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atg tgt agg aaa aga aat gac tac gat gat acc att cca atc ttg gat 1021

Met Cys Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp
305 310 315

gca cta aaa gtc acc gcc aat att gtg ttt gga tat gcc acg tgt caa 1069
Ala Leu Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln
320 325 330

gga gca gaa gct ttt gaa atc cag cat tct gga ttg gca aat gga atc 1117
Gly Ala Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile
335 340 345

ttt atg aaa ttt tta aaa gac aga tta tta gaa gat aag aaa atc act 1165
Phe Met Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr
350 355 360

gtg tta ctg gat gaa gtt gca gaa gat atg ggt aag tgt cac ctt acc 1213
Val Leu Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr
365 370 375 380

aaa ggc aaa cag gct cta gag att cga agt agt tta tct gag aag aga 1261
Lys Gly Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg
385 390 395

gca ctt act gat cca ata cag gga aca gaa tat tct gct gaa tct ctt 1309
Ala Leu Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu
400 405 410

gtg cggtt aat cta cag tgg gcc aag gct cat gaa ctt cca gaa agt atg 1357
Val Arg Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met

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tgt ctt aag ttt gac tgt ggt gtt cag att caa tta gga ttt gca gct 1405
Cys Leu Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala

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gag ttt tcc aat gtc atg atc atc tat aca agt ata gtt tac aaa cca 1453
Glu Phe Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro
445 450 455 460

ccg gag ata ata atg tgt gat gcc tac gtt act gat ttt cca ctt gat 1501
Pro Glu Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp
465 470 475

cta gat att gat cca aaa gat gca aat aaa ggc aca cct gaa gaa act 1549
Leu Asp Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr
480 485 490

ggc agc tac ttg gta tca aag gat ctt ccc aag cat tgc ctc tat acc 1597
Gly Ser Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr
495 500 505

aga ctc agt tca ctg caa aaa tta aag gaa cat cta gtc ttc aca gta 1645
Arg Leu Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val
510 515 520

tgt tta tca tat cag tac tca gga ttg gaa gat act gta gag gac aag 1693
Cys Leu Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys
525 530 535 540

cag gaa gtg aat gtt ggg aaa cct ctc att gct aaa tta gac atg cat 1741

Gln Glu Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His

545

550

555

cga ggt ttg gga agg aag act tgc ttt caa act tgt ctt atg tct aat 1789

Arg Gly Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn

560

565

570

ggc cct tac cag agt tct gca gcc acc tca gga gga gca ggg cat tat 1837

Gly Pro Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr

575

580

585

cac tca ttg caa gac cca ttc cat ggt gtt tac cat tca cat cct ggt 1885

His Ser Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly

590

595

600

aat cca agt aat gtt aca cca gca gat agc tgt cat tgc agc cgg act 1933

Asn Pro Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr

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615

620

cca gat gca ttt att tca agt ttc gct cac cat gct tca tgt cat ttt 1981

Pro Asp Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe

625

630

635

agt aga agt aat gtg cca gta gag aca act gat gaa ata cca ttt agt 2029

Ser Arg Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser

640

645

650

ttc tct gac agg ctc aga att tct gaa aaa tgacctcctt gttttgaaa 2079

Phe Ser Asp Arg Leu Arg Ile Ser Glu Lys

655

660

gttagcataa ttttagatgc ctgtgaaata gtactgcact tacataaagt gagacattgt 2139

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<212> PRT

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<400> 131

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25

30

Leu Arg Glu Pro Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala

35

40

45

Pro Glu Gly Arg Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg

50

55

60

Gly Arg Leu Arg Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys
65 70 75 80

Val Leu Glu Pro Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met
85 90 95

Gly Glu Lys Gly Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala
100 105 110

Met Glu His Thr Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys
115 120 125

Ile Thr Val Asn Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val
130 135 140

Lys Leu Cys Cys Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp
145 150 155 160

Phe Lys Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile
165 170 175

Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val
180 185 190

Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val
195 200 205

Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu
210 215 220

Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro
225 230 235 240

Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro
245 250 255

His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys
260 265 270

Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr
275 280 285

Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val
290 295 300

Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp
305 310 315 320

Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp
325 330 335

Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn
340 345 350

Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu
355 360 365

Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu

370

375

380

Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu

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395

400

Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly

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410

415

Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn

420

425

430

Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu

435

440

445

Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys

450

455

460

Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu

465

470

475

480

Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala

485

490

495

Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met

500

505

510

Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu

515

520

525

Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly

530 535 540

Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu

545 550 555 560

Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg

565 570 575

Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu

580 585 590

Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe

595 600 605

Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu

610 615 620

Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp

625 630 635 640

Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser

645 650 655

Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu

660 665 670

Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu

675 680 685

Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu
690 695 700

Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly
705 710 715 720

Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro
725 730 735.

Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser
740 745 750

Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro
755 760 765

Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp
770 775 780

Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg
785 790 795 800

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Asp Arg Leu Arg Ile Ser Glu Lys
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gggcgggcgg gagccccggc agtccgggt cgccggcgag ggcc atg tcg ctg ttg 176

Met Ser Leu Leu

1

ggg gac ccg cta cag gcc ctg ccg ccc tcg gcc gcc ccc acg ggg ccg 224

Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala Pro Thr Gly Pro

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10

15

20

ctg ctc gcc cct ccg gcc ggc acc ctc aac cgc ctg cgg gag ccg 272

Leu Leu Ala Pro Pro Ala Gly Ala Thr Leu Asn Arg Leu Arg Glu Pro

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ctg ctg cgg agg ctc agc gag ctc ctg gat cag gcg ccc gag ggc cgg 320

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Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg Gly Arg Leu Arg

55 60 65

ctc agt tgc cta gac ctg gag cag tgt tct ctt aag gta ctg gag cct 416
Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys Val Leu Glu Pro
70 75 80

gaa gga agc ccc agc ctg tgt ctg ctg aag tta atg ggt gaa aaa ggt 464
Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met Gly Glu Lys Gly
85 90 95 100

tgc aca gtc aca gaa ttg agt gat ttc ctg cag gct atg gaa cac act 512
Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala Met Glu His Thr
105 110 115

gaa gtt ctt cag ctt ctc agc ccc cca gga ata aag att act gta aac 560
Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys Ile Thr Val Asn
120 125 130

cca gag tca aag gca gtc ttg gct gga cag ttt gtg aaa ctg tgt tgc 608
Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val Lys Leu Cys Cys
135 140 145

cgg gca act gga cat cct ttt gtt caa tat cag tgg ttc aaa atg aat 656
Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp Phe Lys Met Asn
150 155 160

aaa gag att cca aat gga aat aca tca gag ctt att ttt aat gca gtg 704
Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn Ala Val
165 170 175 180

cat gta aaa gat gca ggc ttt tat gtc tgt cga gtt aat aac aat ttc 752
His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn Asn Phe
185 190 195

acc ttt gaa ttc agc cag tgg tca cag ctg gat gtt tgc gac atc cca 800
Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp Ile Pro
200 205 210

gag agc ttc cag aga agt gtt gat ggc gtc tct gaa tcc aag ttg caa 848
Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys Leu Gln
215 220 225

atc tgt gtt gaa cca act tcc caa aag ctg atg cca ggc agc aca ttg 896
Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser Thr Leu
230 235 240

gtt tta cag tgt gtt gct gtt gga agc cct att cct cac tac cag tgg 944
Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr Gln Trp
245 250 255 260

ttc aaa aat gaa tta cca tta aca cat gag acc aaa aag cta tac atg 992
Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu Tyr Met
265 270 275

gtg cct tat gtg gat ttg gaa cac caa gga acc tac tgg tgt cat gta 1040

Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys His Val

280

285

290

tat aat gat cga gac agt caa gat agc aag aag gta gaa atc atc ata 1088

Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile Ile Ile

295

300

305

gga aga aca gat gag gca gtg gag tgc act gaa gat gaa tta aat aat 1136

Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu Asn Asn

310

315

320

ctt ggt cat cct gat aat aaa gag caa aca act gac cag cct ttg gcg 1184

Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro Leu Ala

325

330

335

340

aag gac aag gtt gcc ctt ttg ata gga aat atg aat tac cgg gag cac 1232

Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg Glu His

345

350

355

ccc aag ctc aaa gct cct ttg gtg gat gtg tac gaa ttg act aac tta 1280

Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr Asn Leu

360

365

370

ctg aga cag ctg gac ttc aaa gtg gtt tca ctg ttg gat ctt act gaa 1328

Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu Thr Glu

375

380

385

tat gag atg cgt aat gct gtg gat gag ttt tta ctc ctt tta gac aag 1376

Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Asp Lys

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Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr Arg Ser			
425	430	435	
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Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln Glu Lys			
440	445	450	
gaa act gga ctt aat gtg ttc tta ttg gat atg tgt agg aaa aga aat 1568			
Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys Arg Asn			
455	460	465	
gac tac gat gat acc att cca atc ttg gat gca cta aaa gtc acc gcc 1616			
Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val Thr Ala			
470	475	480	
aat att gtg ttt gga tat gcc acg tgt caa gga gca gaa gct ttt gaa 1664			
Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala Phe Glu			
485	490	495	500
atc cag cat tct gga ttg gca aat gga atc ttt atg aaa ttt tta aaa 1712			
Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe Leu Lys			
505	510	515	

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Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp Glu Val

520 525 530

gca gaa gat atg ggt aag tgt cac ctt acc aaa ggc aaa cag gct cta 1808
Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln Ala Leu
535 540 545

gag att cga agt agt tta tct gag aag aga gca ctt act gat cca ata 1856
Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp Pro Ile
550 555 560

cag gga aca gaa tat tct gct gaa tct ctt gtg cgg aat cta cag tgg 1904
Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu Gln Trp
565 570 575 580

gcc aag gct cat gaa ctt cca gaa agt atg tgt ctt aag ttt gag tgt 1952
Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe Asp Cys
585 590 595

ggt gtt cag att caa tta gga ttt gca gct gag ttt tcc aat gtc atg 2000
Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn Val Met
600 605 610

atc atc tat aca agt ata gtt tac aaa cca ccg gag ata ata atg tgt 2048
Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile Met Cys
615 620 625

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Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp Pro Lys
630 635 640

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Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu Val Ser
645 650 655 660

aag gat ctt ccc aag cat tgc ctc tat acc aga ctc agt tca ctg caa 2192
Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser Leu Gln
665 670 675

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Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr Gln Tyr
680 685 690

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Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn Val Gly
695 700 705

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Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly Arg Lys
710 715 720

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Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln Ser Ser
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Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln Asp Pro

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Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn Val Thr

760

765

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Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe Ile Ser

775

780

785

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Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn Val Pro

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795

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815

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Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu Phe Asp

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Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile Leu Ile

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Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys Ser Leu

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Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val Arg Glu

130 185 140

Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly Asp Thr

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Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg Leu Phe

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Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly Glu Thr

180 185 190

Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr Asn Gly

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Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu Val Arg

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Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn Ser Glu

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Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu Leu Gly

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Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys Leu Pro

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Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn Pro Ala

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455

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Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe Met Lys

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Ala Ser Gly Val Ser Ile Lys Met Ile Thr Gly Asp Ser Gln Glu Thr

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580

585

590

Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln Leu Ser

595

600

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Gln Ile Val Pro Lys Val Ala Val Phe Tyr Arg Ala Ser Pro Arg His

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620

Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val Val Ala

625

630

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640

Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala Ala Asp

645

650

655

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660

665

670

Ala Asp Met Ile Leu Val Asp Asp Asp Phe Gln Thr Ile Met Ser Ala

675

680

685

Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe Val Arg

690

695

700

Phe Gln Leu Ser Thr Ser Ile Ala Ala Leu Thr Leu Ile Ser Leu Ala

705

710

715

720

Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile Leu Trp

725

730

735

Ile Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly Val Glu

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750

Pro Val Asp Lys Asp Val Val Ile Arg Lys Pro Pro Arg Asn Trp Lys Asp

755

760

765

Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser Ser Ile

770

775

780

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785

790

795

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810

815

Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr Lys Ser

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Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr Ala Val

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840

845

Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro Pro Leu

850

855

860

Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu Leu Phe

865

870

875

880

Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile Ile Lys

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ccagtgtggc cgtggctgac actaaagact ttgttagccat caacccgagt gcagttcga 420

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Met Lys Val Ala Arg Phe Gln Lys Ile Pro Asn Gly Glu Asn

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Glu Thr Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu Pro

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Asn Lys Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu

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Phe Asp Ile Ser Glu Asp Glu Pro Leu Trp Lys Tyr Ile Ser Gln

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Val Leu Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile

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115 120 125

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Ser Leu Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val

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Asp Thr Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg

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175 180 185 190

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225 230 235

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Ser Glu Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro
240 245 250

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Lys Thr Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser
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Phe Tyr Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu
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Val Ala Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu
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gct ctt ggt gtt atg aga atg gtg aag aaa agg gcc att gtg aaa aag 1428
Ala Leu Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys
320 325 330

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Leu Pro Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp

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Lys Thr Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe

355 360 365

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Thr Ser Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln

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Val Ile Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu

415 420 425 430

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Ile Ala Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr

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Val Lys Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe

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Met Lys Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln

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Ser Lys Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr

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Gln Gln Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala

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ttg gct tct ggt cct gaa ctg gga cag ctg aca ttt ctt ggc ttg gtg 2052

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gga atc att gat cca cct aga act ggt gtg aaa gaa gct gtt aca aca 2100

Gly Ile Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr

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Val Ala Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala

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895 900 905 910

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Gly Leu Glu Ser Trp Ser Phe Phe Ala Val Tyr Asp Gly His Ala Gly

50 55 60

Ser Gln Val Ala Lys Tyr Cys Cys Glu His Leu Leu Asp His Ile Thr

65 70 75 80

Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly Ala Pro Ser Val Glu Asn

85 90 95

Val Lys Asn Gly Ile Arg Thr Gly Phe Leu Glu Ile Asp Glu His Met

100 105 110

Arg Val Met Ser Glu Lys Lys His Gly Ala Asp Arg Ser Gly Ser Thr

115 120 125

Ala Val Gly Val Leu Ile Ser Pro Gln His Thr Tyr Phe Ile Asn Cys

130 135 140

Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn Arg Lys Val His Phe Phe

145 150 155 160

Thr Gln Asp His Lys Pro Ser Asn Pro Leu Glu Lys Glu Arg Ile Gln

165 170 175

Asn Ala Gly Gly Ser Val Met Ile Gln Arg Val Asn Gly Ser Leu Ala

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Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr Lys Cys Val His Gly Lys

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Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp Asn Met Ser Val Ile Leu

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Ile Cys Phe Pro Asn Ala Pro Lys Val Ser Pro Glu Ala Val Lys Lys

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Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys Arg Val Glu Glu Ile Ile

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Lys Lys Gln Gly Glu Gly Val Pro Asp Leu Val His Val Met Arg Thr

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Glu Lys His Asn Ala Gln Gly Gln Gly Asn Gly Leu Arg Tyr Gly Leu

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Ser Ser Met Gln Gly Trp Arg Val Glu Met Glu Asp Ala His Thr Ala

30 35 40

gtg atc ggt ttg cca agt gga ctt gaa tcg tgg tca ttc ttt gct gtg 617

Val Ile Gly Leu Pro Ser Gly Leu Glu Ser Trp Ser Phe Phe Ala Val

45 50 55

tat gat ggg cat gct ggt tct cag gtt gcc aaa tac tgc tgt gag cat 665

Tyr Asp Gly His Ala Gly Ser Gln Val Ala Lys Tyr Cys Cys Glu His

60 65 70

ttg tta gat cac atc acc aat aac cag gat ttt aaa ggg tct gca gga 713

Leu Leu Asp His Ile Thr Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly

75 80 85 90

gca cct tct gtg gaa aat gta aag aat gga atc aga aca ggt ttt ctg 761

Ala Pro Ser Val Glu Asn Val Lys Asn Gly Ile Arg Thr Gly Phe Leu

95

100

105

gag att gat gaa cac atg aga gtt atg tca gag aag aaa cat ggt gca 809

Glu Ile Asp Glu His Met Arg Val Met Ser Glu Lys Lys His Gly Ala

110

115

120

gat aga agt ggg tca aca gct gta ggt gtc tta att tct ccc caa cat 857

Asp Arg Ser Gly Ser Thr Ala Val Gly Val Leu Ile Ser Pro Gln His

125

130

135

act tat ttc att aac tgt gga gac tca aga ggt tta ctt tgt agg aac 905

Thr Tyr Phe Ile Asn Cys Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn

140

145

150

agg aaa gtt cat ttc ttc aca caa gat cac aaa cca agt aat ccg ctg 953

Arg Lys Val His Phe Phe Thr Gln Asp His Lys Pro Ser Asn Pro Leu

155

160

165

170

gag aaa gaa cga att cag aat gca ggt ggc tct gta atg att cag cgt 1001

Glu Lys Glu Arg Ile Gln Asn Ala Gly Gly Ser Val Met Ile Gln Arg

175

180

185

gtg aat ggc tct ctg gct gta tcg agg gcc ctt ggg gat ttt gat tac 1049

Val Asn Gly Ser Leu Ala Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr

190

195

200

aaa tgt gtc cat gga aaa ggt cct act gag cag ctt gtc tca cca gag 1097

Lys Cys Val His Gly Lys Gly Pro Thr Glu Gln Leu Val Ser Pro Glu

205	210	215	
cct gaa gtc cat gat att gaa aga tct gaa gaa gat gat cag ttc att 1145			
Pro Glu Val His Asp Ile Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile			
220	225	230	
atc ctt gca tgt gat ggt atc tgg gat gtt atg gga aat gaa gag ctc 1193			
Ile Leu Ala Cys Asp Gly Ile Trp Asp Val Met Gly Asn Glu Glu Leu			
235	240	245	250
tgt gat ttt gta aga tcc aga ctt gaa gtc act gat gac ctt gag aaa 1241			
Cys Asp Phe Val Arg Ser Arg Leu Glu Val Thr Asp Asp Leu Glu Lys			
255	260	265	
gtt tgc aat gaa gta gtc gac acc tgt ttg tat aag gga agt cga gac 1289			
Val Cys Asn Glu Val Val Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp			
270	275	280	
aac atg agt gtg att ttg atc tgt ttt cca aat gca ccc aaa gta tcg 1337			
Asn Met Ser Val Ile Leu Ile Cys Phe Pro Asn Ala Pro Lys Val Ser			
285	290	295	
cca gaa gca gtg aag aag gag gca gag ttg gac aag tac ctg gaa tgc 1385			
Pro Glu Ala Val Lys Lys Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys			
300	305	310	
aga gta gaa gaa atc ata aag aag cag ggg gaa ggc gtc ccc gac tta 1433			
Arg Val Glu Glu Ile Ile Lys Lys Gln Gly Glu Gly Val Pro Asp Leu			
315	320	325	330

gtc cat gtg atg cgc aca tta gcg agt gag aac atc ccc agc ctc cca 1481
Val His Val Met Arg Thr Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro

335 340 345

cca ggg ggt gaa ttg gca agc aag agg aat gtt att gaa gcc gtt tac 1529
Pro Gly Gly Glu Leu Ala Ser Lys Arg Asn Val Ile Glu Ala Val Tyr

350 355 360

aat aga ctg aat cct tac aaa aat gac gac act gac tct aca tca aca 1577
Asn Arg Leu Asn Pro Tyr Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr

365 370 375

gat gat atg tgg taaaactgct catctagcca tggagttac cttagacctcc 1629
Asp Asp Met Trp

380

aaaggagagt acagctcaac ttgttgaaa cttaacat ccattctcaa cttaaggaa 1689

ggggatatga catgggtgag aatgattaca tcagagaact tcagcagtac aacagctgc 1749

ccagaactga tttttttttt tttttgtaa atttgagact tatgttaagcg tgattcaaa 1809

ccataattcg tggtaat cagactccag caattttgt tgtatgattt tggttttttg 1869

taaagtgtaa ttgtccttgt acaaaaatgct catatataat tatgaactgc tttaatcac 1929

tatcaaaggtaa acaagaaatg ttggcttat tgtgtatgc aacagatata tagcccttc 1989

aagtcatgtt gtgtttggac ttggggttgg aacagggaga gcagcagcca tgtcagctac 2049

acgctcaa at gtgcagatga ttatggaaaa taacctcaaaa atcttacaaa gctgaacatc 2109

caaggaggtta ttgaaaacta tcttaatgt tcttggtagg ggagttggca ttgttgataa 2169

agccagtc ttcat ttaac tgtctt cag gatgtt cc tt cgttgttcc atgagtattg 2229

caggtaataa tacagtgtat tcataagaat ctcaatcttg gggctaaatg ccttgtttct 2289

tgcacctct ttcaagtcc ttaatatcaa ttactaattg ataaggcagca gtttcctaca 2349

tatagtagga aactgccaca ttttgctat catgattggc tgggcctgct gctgttccta 2409

gtaagatatt ctgaattcca ttttatcaat aaagcttgat ttaacaaaca agaaaactt 2467

<210> 137

〈211〉 358

〈212〉 PRT

<213> Homo sapiens

<400> 137

Met Met Gln Arg Val Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val

1

5

10

15

Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp

20

25

30

Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu

35

40

45

Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val

50

55

60

Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg

65

70

75

80

Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn

85

90

95

Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser

100

105

110

Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser

115

120

125

Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met

130

135

140

Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala

145

150

155

160

Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser

165

170

175

Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr

180

185

190

Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln

195

200

205

Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln

210

215

220

Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro

225

230

235

240

Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gln Gln Pro Thr Ser Gln

245

250

255

Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln

260

265

270

Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr

275

280

285

Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln

290

295

300

Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly

305

310

315

320

Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro

325

330

335

Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln

340

345

350

Pro Gly Pro Gly Tyr Arg

355

<210> 138

<211> 1519

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (11)..(1084)

<400> 138

attagtgcta atg atg caa cga gtt ttc aga gga aaa ctt ctg agt aat 49

Met Met Gln Arg Val Phe Arg Gly Lys Leu Leu Ser Asn

1

5

10

gat gaa gta aca ata aag tat aaa gat gaa gat gga gat ctt ata aca 97

Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr

15

20

25

att ttt gat agt tct gac ctt tcc ttt gca att cag tgc agt agg ata 145

Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile

30

35

40

45

ctg aaa ctg aca tta ttt gtt aat ggc cag cca aga ccc ctt gaa tca 193

Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser

50 55 60

agt cag gtg aaa tat ctc cgt cga gaa ctg ata gaa ctt cga aat aaa 241

Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys

65 70 75

gtg aat cgt tta ttg gat agc ttg gaa cca cct gga gaa cca gga cct 289

Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro

80 85 90

tcc acc aat att cct gaa aat gat act gtg gat ggt agg gaa gaa aag 337

Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys

95 100 105

tct gct tct gat tct tct gga aaa cag tct act cag gtt atg gca gca 385

Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala

110 115 120 125

agt atg tct gct ttt gat cct tta aaa aac caa gat gaa atc aat aaa 433

Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys

130 135 140

aat gtt atg tca gcg ttt ggc tta aca gat gat cag gtt tca ggg cca 481

Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro

145 150 155

ccc agt gct cct gca gaa gat cgt tca gga aca ccc gac agc att gct 529

Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala

160

165

170

tcc tcc tcc tca gca gct cac cca cca ggc gtt cag cca cag cag cca 577
Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Pro

175

180

185

cca tat aca gga gct cag actcaa gca ggt cag atg tac caa cag tac 625
Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr
190 195 200 205

cag caa cag gcc ggc tat ggt gca cag cag ccg cag gct cca cct cag 673
Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln

210

215

220

cag cct caa cag tat ggt att cag tat tca gca agc tat agt cag cag 721
Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln

225

230

235

act gga ccc caa caa cct cag cag ttc cag gga tat ggc cag caa cca 769
Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gln Gln Pro

240

245

250

act tcc cag gca cca gct cct gcc ttt tct ggt cag cct caa caa ctg 817
Thr Ser Gln Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu

255

260

265

cct gct cag ccg cca cag cag tac cag gcg agc aat tat cct gca caa 865
Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln
270 275 280 285

act tac act gcc caa act tct cag cct act aat tat act gtg gct cct 913

Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro

290

295

300

gcc tct caa cct gga atg gct cca agc caa cct ggg gcc tat caa cca 961

Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro

305

310

315

aga cca ggt ttt act tca ctt cct gga agt acc atg acc cct cct cca 1009

Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro

320

325

330

agt ggg cct aat cct tat gcg cgt aac cgt cct ccc ttt ggt cag ggc 1057

Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly

335

340

345

tat acc caa cct gga cct ggt tat cga taaggaggct cctctacacc 1104

Tyr Thr Gln Pro Gly Pro Gly Tyr Arg

350

355

aatttaatgt a gctgcttagt attggcctcc caaaagactc cagtaactatt ttaatttgta 1164

ttgaagaagt tcagaaattt aaaagcagag catttttat gatatcattg ttgggttaa 1224

ttgaaagtat aatttgctgg aacacaaaaga ccaaaatgaa agtttttcc tccctgctta 1284

aaaatgttagc agcttcttag ttactttgga acactactt tacatgtata aagtgattga 1344

cttgactttc tagcttccct tgtccggagg atattaaat gctagggtga ggtttagcca 1404

tcttacttgg cttttacta ttaacatgat gtactaaagt agagccctt gagaatacaa 1464

gatattatgt ataaaatgta acactgatga taggttaata aagatgattg aatcc 1519

<210> 139

<211> 396

<212> PRT

<213> Homo sapiens

<400> 139

Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu Ile Val Lys Ala Gln

1 5 10 15

Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His Asn Glu Asp Ile Thr

20 25 30

Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val Phe Arg Gly Lys Leu

35 40 45

Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp

50 55 60

Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys

65 70 75 80

Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro

85

90

95

Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu

100

105

110

Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu

115

120

125

Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg

130

135

140

Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val

145

150

155

160

Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu

165

170

175

Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val

180

185

190

Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp

195

200

205

Ser Ile Ala Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro

210

215

220

Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr

225

230

235

240

Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala

245

250

255

Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr

260

265

270

Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Phe Gln Gly Tyr Gly

275

280

285

Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro

290

295

300

Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr

305

310

315

320

Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr

325

330

335

Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala

340

345

350

Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr

355

360

365

Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe

370

375

380

Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr Arg

385

390

395

<210> 140

<211> 1641

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (19)..(1206)

<400> 140

aacatcctgg agtccacc atg aac gga cag ttg gat cta agt ggg aag cta 51
Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu
1 5 10

atc gtc aaa gct caa ctt ggg gag gat att cgg cga att cct att cat 99
Ile Val Lys Ala Gln Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His
15 20 25

aat gaa gat att act tat gat gaa tta gtg cta atg atg caa cga gtt 147
Asn Glu Asp Ile Thr Tyr Asp Glu Leu Val Met Met Gln Arg Val
30 35 40

ttc aga gga aaa ctt ctg agt aat gat gaa gta aca ata aag tat aaa 195
Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys
45 50 55

gat gaa gat gga gat ctt ata aca att ttt gat agt tct gac ctt tcc 243

Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser

60 65 70 75

ttt gca att cag tgc agt agg ata ctg aaa ctg aca tta ttt gtt aat 291

Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn

80 85 90

ggc cag cca aga ccc ctt gaa tca agt cag gtg aaa tat ctc cgt cga 339

Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg

95 100 105

gaa ctg ata gaa cit cga aat aaa gtg aat cgt tta ttg gat agc ttg 387

Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu

110 115 120

gaa cca cct gga gaa cca gga cct tcc acc aat att cct gaa aat gat 435

Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp

125 130 135

act gtg gat ggt agg gaa gaa aag tct gct tct gat tct tct gga aaa 483

Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys

140 145 150 155

cag tct act cag gtt atg gca gca agt atg tct gct ttt gat cct tta 531

Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu

160 165 170

aaa aac caa gat gaa atc aat aaa aat gtt atg tca gcg ttt ggc tta 579

Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu

175

180

185

aca gat gat cag gtt tca ggg cca ccc agt gct cct gca gaa gat cgt 627
Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg

190

195

200

tca gga aca ccc gac agc att gct tcc tcc tcc tca gca gct cac cca 675
Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser Ala Ala His Pro

205

210

215

cca ggc gtt cag cca cag cag cca cca tat aca gga gct cag act caa 723
Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln
220 225 230 235

gca ggt cag atg taccaa cag tac cag caa cag ggc tat ggt gca 771
Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Ala Gly Tyr Gly Ala
240 245 250

cag cag ccg cag gct cca cct cag cag cct caa cag tat ggt att cag 819
Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln

255

260

265

tat tca gca agc tat agt cag cag act gga ccc caa caa cct cag cag 867
Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln
270 275 280

ttc cag gga tat ggc cag caa cca act tcc cag gca cca gct cct gcc 915
Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala
285 290 295

ttt tct ggt cag cct caa caa ctg cct gct cag ccg cca cag cag tac 963

Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr

300 305 310 315

cag gcg agc aat tat cct gca caa act tac act gcc caa act tct cag 1011

Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln

320 325 330

cct act aat tat act gtg gct cct gcc tct caa cct gga atg gct cca 1059

Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro

335 340 345

agc caa cct ggg gcc tat caa cca aga cca ggt ttt act tca ctt cct 1107

Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro

350 355 360

gga agt acc atg acc cct cct cca agt ggg cct aat cct tat gcg cgt 1155

Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg

365 370 375

aac cgt cct ccc ttt ggt cag ggc tat acc caa cct gga cct ggt tat 1203

Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr

380 385 390 395

cga taaggaggct cctctacacc aattaatgtt gctgttagct attggcctcc 1256

Arg

caaaagactc cagtactatt ttaatttgtt ttgaagaagt tcagaaattt aaaagcagag 1316

catttttat gatatcattg ttgggttaaa ttgaaagtat aatttgctgg aacacaaaga 1376

ccaaaatgaa agtttttcc tccctgctta aaaatgttagc agcttcttag ttactttgga 1436

acactactt tacatgtata aagtgattga ct tgacttcc tagttccct tgtccggagg 1496

atattaaat gctagggta ggtttagcca tcttacttgg ct tttacta tiaacatgat 1556

gtactaaagt agagcccttt gagaatacaa gatattatgt ataaaatgta acactgatga 1616

taggttaata aagatgattg aatcc 1641

<210> 141

<211> 323

<212> PRT

<213> Homo sapiens

<400> 141

Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro Ala Val Pro

1

5

10

15

Phe Ser Gly Thr Ile Gln Gly Leu Gln Asp Gly Leu Gln Ile Thr

20

25

30

Val Asn Gly Thr Val Leu Ser Ser Gly Thr Arg Phe Ala Val Asn

35

40

45

Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro

50 55 60

Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly

65 70 75 80

Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly

85 90 95

Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val

100 105 110

Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe

115 120 125

His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln Leu Ser Tyr

130 135 140

Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile

145 150 155 160

Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly Gln Met Phe

165 170 175

Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro

180 185 190

Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro Ser Lys Ser

195 200 205

Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg Phe His Ile

210 215 220

Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Pro Arg Phe

225 230 235 240

Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly

245 250 255

Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln

260 265 270

Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala

275 280 285

Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu

290 295 300

Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln Leu Thr His

305 310 315 320

Val Gln Thr

<210> 142

<211> 1616

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (72).. (1040)

<400> 142

aagtgcgttcc ctctacaaaag gacttccttag tgggtgtgaa aggccagcggt ggccacagag 60

gcggcggaga g atg gcc ttc agc ggt tcc cag gct ccc tac ctg agt cca 110

Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro

1

5

10

gct gtc ccc ttt tct ggg act att caa gga ggt ctc cag gac gga ctt 158

Ala Val Pro Phe Ser Gly Thr Ile Gln Gly Leu Gln Asp Gly Leu

15

20

25

cag atc act gtc aat ggg acc gtt ctc agc tcc agt gga acc agg ttt 206

Gln Ile Thr Val Asn Gly Thr Val Leu Ser Ser Gly Thr Arg Phe

30

35

40

45

gct gtg aac ttt cag act ggc ttc agt gga aat gac att gcc ttc cac 254

Ala Val Asn Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His

50

55

60

ttc aac cct cgg ttt gaa gat gga ggg tac gtg gtg tgc aac acg agg 302

Phe Asn Pro Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg

65

70

75

cag aac gga agc tgg ggg ccc gag gag agg aag aca cac atg cct ttc 350
Gln Asn Gly Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe
80 85 90

cag aag ggg atg ccc ttt gac ctc tgc ttc ctg gtg cag agc tca gat 398
Gln Lys Gly Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp
95 100 105

ttc aag gtg atg gtg aac ggg atc ctc ttc gtg cag tac ttc cac cgc 446
Phe Lys Val Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg
110 115 120 125

gtg ccc ttc cac cgt gtg gac acc atc tcc gtc aat ggc tct gtg cag 494
Val Pro Phe His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln
130 135 140

ctg tcc tac atc agc ttc cag cct ccc ggc gtg tgg cct gcc aac ccg 542
Leu Ser Tyr Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro
145 150 155

gct ccc att acc cag aca gtc atc cac aca gtg cag agc gcc cct gga 590
Ala Pro Ile Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly
160 165 170

cag atg ttc tct act ccc gcc atc cca cct atg atg tac ccc cac ccc 638
Gln Met Phe Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro
175 180 185

gcc tat ccg atg cct ttc atc acc acc att ctg gga ggg ctg tac cca 686

Ala Tyr Pro Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro

190

195

200

205

tcc aag tcc atc ctc ctg tca ggc act gtc ctg ccc agt gct cag agg 734

Ser Lys Ser Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg

210

215

220

ttc cac atc aac ctg tgc tct ggg aac cac atc gcc ttc cac ctg aac 782

Phe His Ile Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn

225

230

235

ccc cgt ttt gat gag aat gct gtg gtc cgc aac acc cag atc gac aac 830

Pro Arg Phe Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn

240

245

250

tcc tgg ggg tct gag gag cga agt ctg ccc cga aaa atg ccc ttc gtc 878

Ser Trp Gly Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val

255

260

265

cgt ggc cag agc ttc tca gtg tgg atc ttg tgt gaa gct cac tgc ctc 926

Arg Gly Gln Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu

270

275

280

285

aag gtg gcc gtg gat ggt cag cac ctg ttt gaa tac tac cat cgc ctg 974

Lys Val Ala Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu

290

295

300

agg aac ctg ccc acc atc aac aga ctg gaa gtg ggg ggc gac atc cag 1022

Arg Asn Leu Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln

305

310

315

ctg acc cat gtg cag aca taggcggctt cctggccctg gggccggggg 1070

Leu Thr His Val Gln Thr

320

ctgggtgtg gggcagtctg ggtccctctca tcatccccac ttcccaggcc cagcctttcc 1130

aaccctgcct gggatctggg cttaatgca gagggcatgt ccttgcgtgg tcctgcctct 1190

ggctacagcc acccttggAAC ggagaaggca gctgacgggg attgccttcc tcagcccgAG 1250

cagcacctgg ggctccagct gctggaatcc taccatccca ggaggcaggc acagccaggG 1310

agaggggagg agtgggcagt gaagatgaag ccccatgctc agtccccctcc catccccac 1370

gcagctccac cccagtccta agccaccAGC tgtctgcTCC tggtgggagg tggcctcTC 1430

agccccctcct ctctgaccTT taacctact ctcacCTGC accgtgcACC aacccttCAC 1490

ccctcctgGA aagcaggcCT gatggcttCC cactggcCTC caccacCTGA ccagagtGTT 1550

ctcttcagAG gactggcTCC ttTCCCAGTG tcctaaaAT aaAGAAATGA aaATGCTGT 1610

tggcac

1616

<210> 143

<211> 136

<212> PRT

<213> Homo sapiens

<400> 143

Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile

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Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly

20

25

30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val

35

40

45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val

50

55

60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala

65

70

75

80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile

85

90

95

Pro Leu Pro His Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His

100

105

110

Gly His Leu Ser Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe

115

120

125

Leu Gln Pro Leu Met His Cys Val

130

135

<210> 144

<211> 1252

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (225)..(632)

<400> 144

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cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agtcaccct 180

aaaacattta ttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236

Met Ala Gly Ala

1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284

Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile

5

10

15

20

ctg ctc gtg ttc caa atc atc gcc ttt ctg glg gga ggc ttg att gct 332

Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala

25

30

35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat 380
Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp

40

45

50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc 428
Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro

55

60

65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476
Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu

70

75

80

att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac 524
Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His
85 90 95 100

atg gct ctt agc tgt ggt ttc ttg gac cag cgg cat gga cat ttg tca 572
Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His Gly His Leu Ser

105

110

115

gtt tgc ctt ctg acg gta gct ttt gga gga aga ttc ctg cag cca cta 620
Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe Leu Gln Pro Leu

120

125

130

atg cat tgt gta tgataacaaa aactctggta tgacacatTT tcttgtatca 672
Met His Cys Val
135

tgttaatta gtgacatagt aacatctgta gcagctggtt agtaaacctc atgtgggggt 732

ggggggggg tgtattcctt gggggatggt ttggccgaa tggggagtgg aatatttgac 792

attttcctg tttaaattc taggatagat tttaacatcc ttgcggtcc cagtccaagg 852

taggctgggg tcatacgctt ctcactccta atccatgacc actgtttttt tcctatttat 912

atcaccagggt agcctactga gttaatattt aagttgtcaa tagataagtg tccctgtttt 972

gtggcataat ataactgaat ttcatgagaa gatttattcc accaggggta ttcagcttt 1032

gaaaccaaattt ctgttatct aatactaacc aatctgttgg atgtgggttt taaaaaatgt 1092

ttgctaaact acccaagtaa gatttactgt attaaatggc cttcgggtct gaaaagcttt 1152

ttaacctct tgctaaaaat gcgttttattt ttgataagat acttcaaata gcctccaaaa 1212

gtgttagatcc aatcacttaa ataaacctgt atgtataatgc 1252

<210> 145

<211> 468

<212> PRT

<213> Homo sapiens

<400> 145

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp

1

5

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15

Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Phe

20

25

30

Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln

35

40

45

Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg

50

55

60

Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro

65

70

75

80

Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu

85

90

95

Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser

100

105

110

Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu

115

120

125

Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu

130

135

140

Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met

145

150

155

160

Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp

165

170

175

Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val

180

185

190

Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu

195

200

205

Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp

210

215

220

Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile

225

230

235

240

Phe Cys Gly Glu His Met Met Asp Gln His Glu Arg Asn His Ile Ala

245

250

255

Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu

260

265

270

Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe

275

280

285

Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe

290

295

300

Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys

305

310

315

320

Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser

325

330

335

Leu Pro Ala Met Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile

340

345

350

Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met

355

360

365

Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys

370

375

380

Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile

385

390

395

400

Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala

405

410

415

Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu

420

425

430

Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr

435

440

445

Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala

450

455

460

Ala Ser Gly Ile

465

<210> 146

<211> 1943

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (379)..(1782)

<400> 146

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cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agtcaccct 180

aaaacattt tttcaaggag aaaagaaaaa gggggggcgc aaaaatggct gggcaatta 240

tagaaaacat gagcaccaag aagctgtgca ttgttgtgg gattctgctc gtgttccaaa 300

tcatgcctt tctggggaa ggcttgattt ctccagggcc cacaacggca gtgtcctaca 360

tgtcggtgaa atgtgtgg atg ccc gta aga acc atc aca aga caa aat ggt 411

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly

1

5

10

tcg tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag 459
Ser Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys

15 20 25

agg caa ttc caa ttc atg ctg ttt atc ctg cag ctg gag att gcc ttc 507
Arg Gln Phe Gln Phe Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe
30 35 40

aag cta aac aac caa atc aga gaa aat gca gaa gtc tcc atg gac gtt 555
Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val
45 50 55

tcc ctg gct tac cgt gat gac gcg ttt gct gag tgg act gaa atg gcc 603
Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala
60 65 70 75

cat gaa aga gta cca cgg aaa ctc aaa tgc acc ttc aca tct ccc aag 651
His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys
80 85 90

act cca gag cat gag ggc cgt tac tat gaa tgt gat gtc ctt cct ttc 699
Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe
95 100 105

atg gaa att ggg tct gtg gcc cat aag ttt tac ctt tta aac atc cgg 747
Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg
110 115 120

ctg cct gtg aat gag aag aag aaa atc aat gtg gga att ggg gag ata 795

Leu Pro Val Asn Glu Lys Lys Ile Asn Val Gly Ile Gly Glu Ile

125 130

135

aag gat atc cgg ttg gtg ggg atc cac caa aat gga ggc ttc acc aag 843

Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys

140

145

150

155

gtg tgg ttt gcc atg aag acc ttc ctt acg ccc agc atc ttc atc att 891

Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile

160

165

170

atg gtg tgg tat tgg agg agg atc acc atg atg tcc cga ccc cca gtg 939

Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val

175

180

185

ctt ctg gaa aaa gtc atc ttt gcc ctt ggg att tcc atg acc ttt atc 987

Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile

190

195

200

aat atc cca gtg gaa tgg ttt tcc atc ggg ttt gac tgg acc tgg atg 1035

Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met

205

210

215

ctg ctg ttt ggt gac atc cga cag ggc atc ttc tat gcg atg ctt ctg 1083

Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu

220

225

230

235

tcc ttc tgg atc atc ttc tgt ggc gag cac atg atg gat cag cac gag 1131

Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp Gln His Glu

240

245

250

cgg aac cac atc gca ggg tat tgg aag caa gtc gga ccc att gcc gtt 1179
Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val

255

260

265

ggc tcc ttc tgc ctc ttc ata ttt gac atg tgt gag aga ggg gta caa 1227
Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln

270

275

280

ctc acg aat ccc ttc tac agt atc tgg act aca gac att gga aca gag 1275
Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu
285 290 295

ctg gcc atg gcc ttc atc atc gtg gct gga atc tgc ctc tgc ctc tac 1323
Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr
300 305 310 315

ttc ctg ttt cta tgc ttc atg gta ttt cag gtg ttt cgg aac atc agt 1371
Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser
320 325 330

ggg aag cag tcc agc ctg cca gct atg agc aaa gtc cgg cgg cta cac 1419
Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg Arg Leu His
335 340 345

tat gag ggg cta att ttt agg ttc aag ttc ctc atg ctt atc acc ttg 1467
Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu
350 355 360

gcc tgc gct gcc atg act gtc atc ttc ttc atc gtt agt cag gta acg 1515
Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr

365 370 375

gaa ggc cat tgg aaa tgg ggc ggc gtc aca gtc caa gtg aac agt gcc 1563
Glu Gly His Trp Lys Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala
380 385 390 395

ttt ttc aca ggc atc tat ggg atg tgg aat ctg tat gtc ttt gct ctg 1611
Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu
400 405 410

atg ttc ttg tat gca cca tcc cat aaa aac tat gga gaa gac cag tcc 1659
Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser
415 420 425

aat gga atg caa ctc cca tgt aaa tcg agg gaa gat tgt gct ttg ttt 1707
Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe
430 435 440

gtt tcg gaa ctt tat caa gaa ttg ttc agc gct tcg aaa tat tcc ttc 1755
Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe
445 450 455

atc aat gac aac gca gct tct ggt att tgagtcaaca aggcaacaca 1802
Ile Asn Asp Asn Ala Ala Ser Gly Ile
460 465

tgttatcag cttgcattt gcagttgtca cagtcacatt gatgtactt gtatacgac 1862

acaatacac tcatttagcc ttatctcaa aatgttaat ataaggaaaa aagcgtcaac 1922

aataaatatt ctttgagtat t 1943

<210> 147

<211> 460

<212> PRT

<213> Homo sapiens

<400> 147

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp

1 5 10 15

Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Gly

20 25 30

Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr Phe Pro Ser Pro

35 40 45

Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr

50 55 60

Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr

65 70 75 80

Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val

85

90

95

Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu

100

105

110

Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile

115

120

125

Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly

130

135

140

Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile

145

150

155

160

Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg

165

170

175

Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met

180

185

190

Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp

195

200

205

Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala

210

215

220

Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp

225

230

235

240

Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro

245 250 255

Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg

260 265 270

Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile

275 280 285

Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu

290 295 300

Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg

305 310 315 320

Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg

325 330 335

Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu

340 345 350

Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser

355 360 365

Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile Thr Val Gln Val

370 375 380

Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val

385 390 395 400

Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu
405 410 415

Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys
420 425 430

Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys
435 440 445

Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile
450 455 460

<210> 148

<211> 1919

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (376)..(1755)

<400> 148

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agaaaggagg cgaggaagga gggagtgtat gagaggaggg agcaaaaAGC tcaccctaaa 180

acatttattt caaggagaaa agaaaaaggg ggggcgcaaa aatggctggg gcaattata 240

aaaacatgag caccaagaag ctgtgcattt tgggtggat tcgtcgtt ttccaaatca 300

tgcctttct ggtgggaggc ttgattgctc cagggcccac aacggcagtg tcctacatgt 360

cggtgaaatg tgigg atg ccc gta aga acc atc aca aga caa aat ggt tcg 411

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser

1

5

10

tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag agg 459

Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg

15

20

25

caa ttc caa ggg aaa ttg aag cca atg aca tcg tgt ttt ctg ttc aca 507

Gln Phe Gln Gly Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr

30

35

40

ttc ccc tcc ccc atg gac gtt tcc ctg gct tac cgt gat gac gcg ttt 555

Phe Pro Ser Pro Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe

45

50

55

60

gct gag tgg act gaa atg gcc cat gaa aga gta cca cggtt aca 603

Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys

65

70

75

tgc acc ttc aca tct ccc aag act cca gag cat gag ggc cgt tac tat 651

Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr

80

85

90

gaa tgt gat gtc ctt cct ttc atg gaa att ggg tct gtg gcc cat aag 699
Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys

95

100

105

ttt tac ctt tta aac atc cgg ctg cct gtg aat gag aag aag aaa atc 747
Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile
110 115 120

aat gtg gga att ggg gag ata aag gat atc cgg ttg gtg ggg atc cac 795
Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His
125 130 135 140

caa aat gga ggc ttc acc aag gtg tgg tti gcc atg aag acc ttc ctt 843
Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu
145 150 155

acg ccc agc atc ttc atc att atg gtg tgg tat tgg agg agg atc acc 891
Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr
160 165 170

atg atg tcc cga ccc cca gtg ctt ctg gaa aaa gtc atc ttt gcc ctt 939
Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu
175 180 185

ggg att tcc atg acc ttt atc aat atc cca gtg gaa tgg ttt tcc atc 987
Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile
190 195 200

ggg ttt gac tgg acc tgg atg ctg ctg ttt ggt gac atc cga cag ggc 1035

Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly

205 210 215 220

atc ttc tat gcg atg ctt ctg tcc ttc tgg atc atc ttc tgt ggc gag 1083

Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu

225 230 235

cac atg atg gat cag cac gag cgg aac cac atc gca ggg tat tgg aag 1131

His Met Met Asp Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys

240 245 250

caa gtc gga ccc att gcc gtt ggc tcc ttc tgc ctc ttc ata ttt gac 1179

Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp

255 260 265

atg tgt gag aga ggg gta caa ctc acg aat ccc ttc tac agt atc tgg 1227

Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp

270 275 280

act aca gac att gga aca gag ctg gcc atg gcc ttc atc atc gtg gct 1275

Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe Ile Val Ala

285 290 295 300

gga atc tgc ctc tgc ctc tac ttc ctg ttt cta tgc ttc atg gta ttt 1323

Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe

305 310 315

cag gtg ttt cgg aac atc agt ggg aag cag tcc agc ctg cca gct atg 1371
Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met

320 325 330

agc aaa gtc cgg cgg cta cac tat gag ggg cta att ttt agg ttc aag 1419
Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys

335 340 345

ttc ctc atg ctt atc acc ttg gcc tgc gct gcc atg act gtc atc ttc 1467
Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe

350 355 360

ttc atc gtt agt cag gta acg gaa ggc cat tgg aaa tgg ggc ggc atc 1515
Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile
365 370 375 380

aca gtc caa gtg aac agt gcc ttt ttc aca ggc atc tat ggg atg tgg 1563
Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp
385 390 395

aat ctg tat gtc ttt gct ctg atg ttc ttg tat gca cca tcc cat aaa 1611
Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys
400 405 410

aac tat gga gaa gac cag tcc aat gga atg caa ctc cca tgt aaa tcg 1659
Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser
415 420 425

agg gaa gat tgt gct ttg ttt gtt tcg gaa ctt tat caa gaa ttg ttc 1707

Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe

430 435 440

agc gct tcg aaa tat tcc ttc atc aat gac aac gca gct tct ggt att 1755

Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile

445 450 455 460

tgagtcaaca aggcaacaca tgtttatcag ctttgattt gcagttgtca cagtcacatt 1815

gattgtactt gtatacgcac acaaaatacac tcatttagcc ttatctcaa aatgttaaat 1875

ataaggaaaa aagcgtcaac aataaatatt ctttgagtat tgtc 1919

<210> 149

<211> 183

<212> PRT

<213> Homo sapiens

<400> 149

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro

1 5 10 15

Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile

20 25 30

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val

35 40 45

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val

50 55 60

Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr

65 70 75 80

Glu Glu Arg Ser Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu

85 90 95

Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val

100 105 110

Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn

115 120 125

Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser

130 135 140

Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala

145 150 155 160

Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe

165 170 175

Asp Arg His Lys Met Leu Ser

180

<210> 150

<211> 1562

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<213> Homo sapiens

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<221> CDS

<222> (120).. (668)

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ttgcggctgc agcgggcttg taggtgtccg gccttgcgtgg cccagcaagc ctgataagc 119

atg aag ctc tta tct ttg gtg gct gtc ggg tgt ttg ctg gtg ccc 167

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro

1

5

10

15

cca gct gaa gcc aac aag agt tct gaa gat atc cgg tgc aaa tgc atc 215

Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile

20

25

30

tgt cca cct tat aga aac atc agt ggg cac att tac aac cag aat gta 263

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val

35

40

45

tcc cag aag gac tgc aac tgc ctg cac gtg gtg gag ccc atg cca gtg 311

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val

50

55

60

cct ggc cat gac gtg gag gcc tac tgc ctg ctg gag tgc agg tac 359
Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
65 70 75 80

gag gag cgc agc acc acc acc atc aag gtc atc att gtc atc tac ctg 407
Glu Glu Arg Ser Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
85 90 95

tcc gtg gtg ggt gcc ctg ttg ctc tac atg gcc ttc ctg atg ctg gtg 455
Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
100 105 110

gac cct ctg atc cga aag ccg gat gca tat act gag caa ctg cac aat 503
Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
115 120 125

gag gag gag aat gag gat gct cgc tct atg gca gca gct gct gca tcc 551
Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser
130 135 140

ctc ggg gga ccc cga gca aac aca gtc ctg gag cgt gtg gaa ggt gcc 599
Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
145 150 155 160

cag cag cgg tgg aag ctg cag gtg cag gag cag cgg aag aca gtc ttc 647
Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
165 170 175

gat cgg cac aag atg ctc agc tagatggcgt ggtgtggtttg ggtcaaggcc 698

Asp Arg His Lys Met Leu Ser

180

ccaacaccat ggctgccagc ttccaggctg gacaaagcag gggctactt ctcccttccc 758

tcggttccag tcttcccttt aaaaggcctgt ggcatttttc ctcccttccc ctaacttttag 818

aaatgttgta cttggctatt ttgatttaggg aagagggatg tggtctctga tctccgttgt 878

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tcgaggcggc ctcaggagtg gatgcgatct gtctctcctg gtcactct tgccgccttc 998

cagctctgag tcttggaaat gtgttaccc ttggaagata aagctgggtc ttcaagaaact 1058

cagtgtctgg gaggaagca tggccagca ttcaagcatgt gtccctttct gcagtggttc 1118

tttatcacca ctcctcccc agccccagcg ctcagcccc agccccagct ccagccctga 1178

ggacagctct gatgggagag ctggcccccc tggccact ggtctttag ggtgcactgg 1238

aagctggtgt tcgttgtccc ctgtgcactt ctgcactgg ggcattggagt gcccatgcat 1298

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gtgtccacag tcactgagcc agacggtcgg ttggaacatg agactcgagg ctgagcgtgg 1418

atctgaacac cacagccccct gtaatgggt tgcctttgt ccctgaactt cgttgtacca 1478

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tcattaaatt gtttttatttc tctc 1562

<210> 151

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

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<210> 152

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 152

cgacctgcag ctgcgagcaca 20

FIG.1

